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Db 709 CACATTTTGGAGCATTATATCACTGCTCCAAAGCTTATGAACGGAAGTTGCAACAG 768
Qy 61 AspLysValIleuIleTherGluLeuIleGlnHisSerAlaIysHisLysValAspIleAsn 80
Db 769 GACAAAGTTTATATACAGAGCTCATCCAGCATTCAGCAAAACATTAAGGTGACATTTAT 828
Qy 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 829 TGCACTGACGAAGGTTGTAGTTTACAGTCAAAAGCTCCCAAGAGTTGGCTCTCTCTTCA 888
Qy 101 AspCysPheLeuThValIleuLeuGlyLysLeuGlyLysSerPheAsnSerValHisLeu 120
Db 889 GACTGTTTCTCACAGTACTCTCGGGTAAACTGGAGAAAGAGCTCAACTGTTCACTGACCTG 948
Qy 121 LeuAlaGlyLysPheAlaGlnPheSerArgCysPheProGlyLeuCysGlyGlyLysSer 140
Db 949 CTTCAGAGTGGGTTGGCTGAGTTCCTCGTGTGTTCCTCGGCTCTGTGAGAGAAATCC 1008
Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTTAGTCCCTACCTGACATTTCTCAGCCTTGCTTACCTGTTGCCAATTTGGGCAAC 1068
Qy 161 ArgIleLeuProAsnLeuTyrIleuGlyCysGlnAspValLeuAsnLysGlyLeuIle 180
Db 1069 CGAATTCCTCCCAATCTTATCTTGGCTGCCAGCAGAGATGCTTCACAAAGAGCTGATG 1128
Qy 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
Db 1129 CAGCGAATGGGATTTGTTATGTGTTAAATGCCAAATACCTGTGCCAAAGCTGACCTT 1188
Qy 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlyLysIleLeu 220
Db 1189 ATCCCGAGCTCATTTCTCGGTGTGCTCGAATGACAGCTTTTGAGAAATTTTG 1248
Qy 221 ProTrpLeuAspLysSerValAspPheIleGlyLysAlaLysAlaSerAsnGlyCysVal 240
Db 1249 CCGGTGTGGAACAATCAGTATTCATTGAGAAAGCAAAAGCTCCAAATGATGTGT 1308
Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 1309 CTAGTGCACTGTTTATAGTGGATCTCCGCTCCGCCACCACTGCTATGCTTACATCATG 1368
Qy 261 LysArgMetAspMetSerLeuAspGlnAlaTyrArgPheValLysGlyLysArgProThr 280
Db 1369 AAGGAGATGGACATGCTTATGATGAGCTTACAGATTTTGAAAGAAAGAAAGACTACT 1428
Qy 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlyLysLysIleLysAsn 300
Db 1429 ATATCTCCAAACTTCAATTTCTGGGCCCACTCTGACATATGAGAAAGATTTAAGAAC 1488
Qy 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlnLysProAsn 320
Db 1489 CAGACTGGAGCATGAGGCCAAAGCAAAAGCAACTCAAGCTGCTGACCTGGAGAAACCAAT 1548
Qy 321 GluProValProAlaValSerGlyGlyGlnLysSerGlnThrProLeuSerProPro 340
Db 1549 GAACCTGTCCCTGCTGTCTCAGAGGTGACAGAAAGAGAGAGCCCTCAGTCCACCC 1608
Qy 341 CysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnLysProValHisProAlaSerVal 360
Db 1609 TGTGCCCACTGTGCTACCTCAGAGGACAGCAAGAAAGCCCGGACATCCCGCAGCGTG 1668
Qy 361 ProSerValProSerValGlnProSerLeuGlnLysAspSerProLeuValGlnAlaLeu 380
Db 1669 CCGAGCGTCCGACCGTGGACCCCTGCTGTTAAGAGACAGCCCGCTGGTACAGGCCCTC 1728
Qy 381 SerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerAsnLysLeuLysArgSerPhe 400
Db 1729 AGTGGCTGCACTGTCCGACAGAGCTGGAAGACAGCAATTAAGCTCAAGCGTTCTTC 1788
Qy 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
Db 1789 TCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGATCTTACATGCTTC 1848
Qy 421 SerSerSerGlnAspAlaLeuGlnTyrTyrIleProSerThrThrIleAspGlyThrAsn 440
Db 1849 TCTCATCAGAAAGTGTCTTGGAAATCTTACAAACTTTCACATCTGTGATGGGACCAAC 1908
Qy 441 LysLeuCysGlnPheSerProValGlnLysLeuSerGlnLysThrProGlnThrSerPro 460
Db 1909 AAGCTTAGCCAGTTCTCCCTGTTCAAGAACTATCGAGAGAGACTCCCGAAACAGCTCT 1968
Qy 461 AspLysGlnLysAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db 1969 GATTAAGAGAGAGCAGCATCCCAAGAACTGACAGACCCGAGGCTTACAGACAGCAG 2028
Qy 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyLysArgPheLeuLeu 500
Db 2029 AGCAAGGATTTGACATTCGTGACAGAACAGACAGAGTGGCACCCGCCAGAGTCCCTTTA 2088
Qy 501 SerProLeuHisArgSerGlySerValGlnAspAsnTyrHisThrSerPheLeuPheGly 520
Db 2089 TCTCAGCTGATGGAAGTGGAGGAGGTGAGAGACATTAACACACAGCTTCTTTTCGGC 2148
Qy 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLysGlyTyrTrpHis 540
Db 2149 CTTTCCACAGCAGCAGCAGCACTCACGAAGTCTGTGGCTGGGCTTAAAGGCTGGCAC 2208
Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTrpPheAla 560
Db 2209 TCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGTGATTTTGGC 2268
Qy 561 ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerAlaSerTyrSer 580
Db 2269 ACAAGATCTCACAACCTTCTACTGCTCAGCATCTCAGGAGGAGTGCACATTACTCT 2328
Qy 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValLysSerValArgArgArg 600
Db 2329 GCCTTACAGCTGACAGCAGCTCCACTTGGGAGAACCAACTTATCTGTGCGCAGGCGG 2388
Qy 601 GlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGlnGlnSerProPheGln 620
Db 2389 CAGAGCGCAATGACAGAGCTGACTGCTGGCGGAGCTGGCATAAAGAGACCCCTTTGAA 2448
Qy 621 LysGlnPheLysArgArgSerCysGlnMetGlnPheGlyGlnSerIleMetSerGlnAsn 640
Db 2449 AACGAGTTTAAAGCAGAGAGCTGCCAAATGGAATTTGAGAGAGCATATGTCAGAGAAC 2508
Qy 641 ArgSerArgGlnLysLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGln 660
Db 2509 AGGTCAAGGGAAGAGCTGGGGAAGTGGGCAATGACTTTCGGGCGAGCATGGAA 2568
Qy 661 IleIleGlnValSer 665
Db 2569 ATCATTTAGGTTCTCC 2583
Db 2569 ATCATTTAGGTTCTCC 2583
RESULT 2
ABV21316
ID ABV21316 standard; cDNA; 5145 BP.
XX
AC ABV21316;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 21307.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN NC200160860-A2.
XX
PD 23-ANG-2001.
XX
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PF 20-FEB-2001; 2001WO-US005171.  
XX  
XX 17-FEB-2000; 2000US-0183319P.  
PR 16-MAR-2000; 2000US-0189862P.  
PR 25-MAY-2000; 2000US-0207454P.  
PR 09-JUN-2000; 2000US-0211314P.  
PR 18-JUL-2000; 2000US-0219007P.  
PR 13-DEC-2000; 2000US-0255281P.  
XX  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
XX Schlegel R, Endege WO, Monahan JE;  
XX  
XX WPI; 2001-662795/76.  
XX  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.  
XX  
XX Claim 1; Page 3540; 11750DP; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABY00010-ABY62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX  
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;  
  
Alignment Scores:  
Pred. No.: 0 Length: 5145  
Score: 3406.00 Matches: 663  
Percent Similarity: 99.85% Conservative: 1  
Best Local Similarity: 99.70% Mismatches: 0  
Query Match: 99.65% Indels: 0  
DB: 1 Gaps: 0  
  
US-10-029-345A-109 (1-665) X ABV21316 (1-5145)  
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluLeuValAlaLeuLeuGlu 20  
DB 589 ATGGCCCATGAGATGATTGGAAGCTCAAAATGTTACTGAGAGGTTGGCTGCTGGAA 648  
QY 21 SerGlyThrGluLeuValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40  
DB 649 AGTGAAGCAAGAAAGAGCTGCTAAATGATAGCGGCGCATTTGGAGAAATCAATACATCC 708  
QY 41 HisIleLeuGlnAlaIleAsnIleAsnCySerLeuLeuMetCysArgArgLeuGln 60  
DB 709 CACATTTTGAACCATTAATATCACTGCTCAAGCTTATGAAGAGAGAGTTGCAACAG 768  
QY 61 AspLeuValLeuIleThrGluLeuIleGlnHisSerAlaIleValIleValIleAsp 80  
DB 769 GACAAAGGTGTAATTCAGAGCTCATCCACATTCAGCGAAGCAATAGGTTGACATTTGAT 828  
QY 81 CysSerGlnIleValValIleTyrAspGlnSerSerGlnAspValIleSerLeuSerSer 100  
DB 829 TGCAGTCAGAAAGTTGATTACGATCAAGCTCCCAAGATGTGCTCTCTCTCTCA 888  
QY 101 AspCysPheLeuThrValIleLeuGluIleValIleValIleValIleValIleVal 120  
DB 889 GACGTGTTTCTCACTGATCTTCTGGGTAACCTGGAGAAAGAGCTTCAACTCTGTTCACTG 948  
QY 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGluLeuCysGluGlyIleVal 140  
DB 949 CTTCAGAGTGGTGTGCTGATCTCTCTGTTTCCCTGGCTCTGTGAGAGAAATCC 1008

QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160  
DB 1009 ACTGTAGTCCCTTAACCGATTTCTCGACCTGTGTTACTGTTCCAAATGGGCCAACCC 1068  
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnIleGluLeu 180  
DB 1069 CGAATTCCTCCCAATCTTATCTTGGCTGCGACGAGAGATGCTCTCAAGAGAGCTGATG 1128  
QY 181 GlnGlnAsnGlyIleGlyTyrValIleAsnAlaSerTyrThrCysProIleAspPhe 200  
DB 1129 CAGCAAAATGGAGATGTTATGTTAAATGCGAAGATACCTGTCAAAGCTGACTTT 1188  
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluIleLeu 220  
DB 1189 ATCCCGAGTCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1248  
QY 221 ProTyrLeuAspIleSerValAspPheIleGluValAlaIleValAsnGlyCysVal 240  
DB 1249 CCGTGGTTGGACAAATCAGTATGATTTCAATTGAGAAAGCAAAAGCTTCAATGATGTT 1308  
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260  
DB 1309 CTAGTCACTGTTTACTGAGATCTCCGCTCGCAACATGCTATCGCTACATCATG 1368  
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluIleValArgProThr 280  
DB 1369 AGAGAGATGACATGCTTATGATGAGCTTACAGATTTGTGAAGAAAAAAGCACTACT 1428  
QY 281 IleSerProAsnPheAsnPheLeuGlyIleLeuLeuAspTyrGluIleValIleVal 300  
DB 1429 ATATCTCCAACTTCATTTTCTGGGCCCAACTCTGAGCTATGAGAAAGATTAAGAAC 1488  
QY 301 GlnThrGlyAlaSerGlyProIleSerIleValLeuLeuIleGlnIleValProAsn 320  
DB 1489 CAGACTGAGACATCAGAGCCAAAGAGCAAACTAACTGCTGAGCTGAGAGCAAAAT 1548  
QY 321 GluProValProAlaValSerGluGlyIleGlnIleSerGluThrProLeuSerProPro 340  
DB 1549 GAACCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1608  
QY 341 CysAlaAspSerAlaThrSerGluAlaIleGlyIleGlnArgProValHisProAlaSerVal 360  
DB 1609 TGTGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1668  
QY 361 ProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAlaLeu 380  
DB 1669 CCCAGGTGCCAGCGCTGAGCGCTGCTGTTAGAGAGACGCCGCTGTAACAGCGCTC 1728  
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnIleValIleValIleVal 400  
DB 1729 AGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1788  
QY 401 SerLeuAspIleIleSerValSerTyrSerAlaSerMetAlaIleSerLeuHisGlyPhe 420  
DB 1789 TCTCTGATATCAATCAATGATTTATTCATGTCAGCAGATGGACATCTTACATGCTTC 1848  
QY 421 SerSerSerGlnAspAlaLeuGluTyrTyrIleValProSerThrThrLeuAspGlyThrAsn 440  
DB 1849 TCTCTCATCAGAAATCTTGGTAATCTCAAACTTCACTGATGTTGAGACCAAC 1908  
QY 441 LysLeuCysGlnPheSerProValGlnIleSerGluIleGlnThrProGluThrSerPro 460  
DB 1909 AAGCTATGCCAGTCTTCCCTGTTCAAGAACTATCGAGAGAGCTCCCAAGAACAGCTCT 1968  
QY 461 AspLeuGluGluAlaSerIleProIleValIleGlnIleThrAlaArgProSerAspSerGln 480  
DB 1969 GATTAAG 2028  
QY 481 SerIleArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500  
DB 2029 AGCAAGCGATGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2088

QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520  
DB 2089 TCTCCACCTGCATCGAAGTGGAGCGGTGGAGGACAAATTACCAACAGCTTCTTTCCGAC 2148  
QY 521 LeuSerThrSerGlnHisIleuThrIleuSerAlaGlyLeuGlyIleuLysGlyTyrHis 540  
DB 2149 CTTTCACCGACGACGACCTTACGAAAGTGTGCTGGCTGGGCTTAAAGGGCTGGGAC 2208  
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTyrPheAla 560  
DB 2209 TCGGATATCTTGGCCCCCAGACCTTACCCCTTCCGACGACGACGCTGGATTTTCC 2268  
QY 561 ThrGluSerSerHisPheTyrSerIleAspAlaIleTyrGlyGlySerAlaSerTyrSer 580  
DB 2269 ACAGAGCTCTCACCTTACTCTCTCCCTCAGCCATCTCAGGAGGAGGAGCCAGTTACTCT 2328  
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600  
DB 2329 GCTTACAGCTGAGCAGCTGCGCACTTGCAGGAGCAAGCTTATTTGTGGCGAGGGCG 2388  
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrPheIleGlnGluSerProPheGlu 620  
DB 2389 CAGAAAGCAAGTGAAGAGAGTGAATCTCGCGCGAGCTGGCATGAAGAGAGCCCTTTGAA 2448  
QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAsn 640  
DB 2449 AAGCAGTTTAAACGACGAAGCTGCCCAATGGATTTGGAGAGAGCATCATGTACAGAAC 2508  
QY 641 ArgSerArgGlnGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660  
DB 2509 AGGTACCGGGAAGAGCTGGGGAAGTGGGAGTCACTTACGCTTTTCCGGGACGATGAA 2568  
QY 661 IleIleGluValSer 665  
DB 2569 ATCATTTGAGGTCTCC 2583

## RESULT 3

ABV26826  
ID ABV26826 standard; cDNA; 5145 BP.

XX AC ABV26826;  
XX 16-SEP-2002 (first entry)  
XX Human prostate expression marker cDNA 26817.  
XX DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX KW pharmacogenomic marker; gene; ss.  
XX OS Homo sapiens.  
XX PN MO200160860-A2.  
XX 23-AUG-2001.  
XX 20-FEB-2001; 2001WO-US005171.  
XX 17-FEB-2000; 2000US-0183319P.  
XX 16-MAR-2000; 2000US-0189862P.  
XX 25-MAY-2000; 2000US-0207454P.  
XX 09-JUN-2000; 2000US-0211314P.  
XX 18-JUL-2000; 2000US-0219007P.  
XX 13-DEC-2000; 2000US-0255281P.  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 5420-5421; 11750bp; English.  
PS The invention relates to an isolated nucleic acid molecule (I) comprising  
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing whether prostate cancer has metastasized in a patient; (g)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX  
SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;  
Alignment Scores:  
Pred. No.: 0 Length: 5145  
Score: 3406.00 Matches: 663  
Percent Similarity: 99.85% Conservative: 1  
Best Local Similarity: 99.70% Mismatches: 1  
Query Match: 99.65% Indels: 0  
DB: 1 Gaps: 0  
US-10-029-345a-109 (1-665) x ABV26826 (1-5145)  
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20  
DB 589 ATGGCCCATAGATGATGTGAACTCAAAATTTGTTACTGAGAGGTTGGTCTGCTCGCGAA 648  
QY 21 SerGlyThrGlnLysValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40  
DB 649 AGTGAAGCAAAAGAGTGGCTGCTATTTGATGATGCGCGCATTTTGGAAATACATACATCC 708  
QY 41 HisIleLeuGluAlaIleAsnIleAsnCysSerLysLeuMetLysArgArgLeuGlnGln 60  
DB 709 CACATTTTGGAAAGCATTAATATCACTGCTCCAACTTATGAAGGAGGTTGCAACAG 768  
QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysIleValAspIleAsp 80  
DB 769 GACAAAGTGTAAATTCAGAGCTCATTCAGCATTCAGCAAAATGAAGTTGACATTGAT 828  
QY 81 CysSerGlnLysValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100  
DB 829 TCGAGTCAGAGGTTGATTTGATTCGATCAAGCTCCCAAGATTTGCTCTCTCTTCA 888  
QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120  
DB 889 GACTGTTTCTCACTGACTTCTGGGTTAACTGAGAAAGGCTTCAACTCTGTTCACTG 948  
QY 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuLysGlnGlyLysSer 140  
DB 949 CTTCAGAGTGGGTTTCTGAGATCTCTGTTGTTCTCTGCGCTCTGTAAAGAAATATCC 1008  
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160  
DB 1009 ACTCTAGTCCCTACCTCGCATTTCTGACCTTGTCTTACCTGTTGCCAACTTGGGCCAAC 1068  
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180  
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QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220  
DB 1189 ATCCCGGATCTCATTTCTGCGTGGCTGCTGATGACAGCTTTTGTGAGAAATTTTG 1248  
QY 221 ProTyrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240



## Alignment Scores:

Pred. No.: 0 Length: 5145  
Score: 3406.00 Matches: 663  
Percent Similarity: 99.85% Conservative: 1  
Best Local Similarity: 99.70% Mismatches: 1  
Query Match: 99.65% Indels: 0  
DB: 1 Gaps: 0

US-10-029-345a-109 (1-665) x ABV27131 (1-5145)

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DB 569 AAGGCCCATGAGATATTGGAACCAAAATGTTACTGAGAGGTTGGTGGCTCTGCTGGA 648  
QY 21 SerGlyThrGluValLeuLeuLeuIleAspSerAaGpProPheValGluTyraAsnThrSer 40  
DB 649 AOTGAGAGGAAAAAGTCTGCTAATTGATAGCCGGCAATTTGTGAATACAAATACATCC 708  
QY 41 HisIleLeuGluAlaIleAsnIleAsnCySerIlyLeuMetLysArgArgLeuGln 60  
DB 709 CACATTTGGAAAGCCATTAAATATCAATGCTCCCAAGCTTTATGAAGCGAAGGTGCAACG 768  
QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisValAspIleAsp 80  
DB 769 GACCAAGGTTAATATACAGAGCTCATCCAGCATTCAGGAAACATTAAGGTTGACATTGAT 828  
QY 81 CysSerGlnLysValValValValTyraSpGlnSerSerGlnAspValAlaSerLeuSerSer 100  
DB 829 TGCAGTCAGAAAGGTTGATGTTTACATCAAAAGCTCCCAAGATGTTGGCTCTCTCTTCA 888  
QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120  
DB 889 GACTGTTTTCACAGTACTTCTGGGTAACTGGAGAAAGACCTTCAACTCTGTTCACTG 948  
QY 121 LeuAlaGlyLysPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140  
DB 949 CTTCAGAGTGGGTTTCTGAGTTCTCTGTGTTTCCCTGGCTCTGTGAAGAAATCC 1008  
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160  
DB 1009 ACTCTAGTCCCTACCTGCAATTTCTCAGCTTTCAGCTTCTGTTGCAACATTTGGCCAA 1068  
QY 161 ArgIleLeuProAsnLeuTyrrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180  
DB 1069 CGAATCTTCCCAATCTTATCTGGCGCCAGAGATGTCCTCAACAAGAGACTGATG 1128  
QY 181 GlnGlnAsnGlyIleGlyTyrrValLeuAsnAlaSerTyrrCysProLysProAspPhe 200  
DB 1129 CAGCAGAAATGGGATTTGTTATGTGTTAAATCCAGCAATACCTGTCCAAAGCTGACTTT 1188  
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QY 221 ProThrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240  
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DB 1309 CTATGTGACCTGTTTAACTGGGATCTCCCGCTCCGCCACCAATCGCTATCGCTACATG 1368  
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyraArgPheValLysGluLysArgProThr 280  
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DB 1429 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGACATATGGAAGAAAGATTAAAC 1488  
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DB 1489 CAGACTGAGATCAGGGGCCAAAGAGCAACTCAAGCTGTGACCTGGAGAAAGCCAAAT 1548

QY 321 GluProValProAlaValSerGluGlyGlyLysSerGluThrProLeuSerProPro 340  
DB 1549 GAACCTTCTCCCTGTGCTTCAAGAGGGGAGACAGAAAAGCCAGAGCCCTTCAGTCCACC 1608  
QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360  
DB 1609 TGTGCCACTCTGTACTCAGAGGCGCAGAGCAAAAGCCCGTGCATCCCGCAGGCTG 1668  
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380  
DB 1669 CCCAGCTGCGCCAGCGCGCAGCCGCTGTATAGAGCACGCCGCTGTACAGGCGCTC 1728  
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe 400  
DB 1729 AGTGGCTGCACCTGTCCGACAGAGCTGGAAGACAGCAATAGCTCAAGCGTTCTTC 1788  
QY 401 SerLeuAspIleLysSerValSerTyrrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420  
DB 1789 TCTCTGGATATCAAAATCAGTTTCAATATTCAGCAGATGGCAGCATCTTACATGGCTTC 1848  
QY 421 SerSerSerGluAspAlaLeuGluTyrrTyrrLysProSerThrThrLeuAspGlyThrAsn 440  
DB 1849 TCCTCATCAGAAAGATGCTTGGAAATCTCAAACTTCCACTGCTGATGGAGCAAC 1908  
QY 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460  
DB 1909 AAGCTATGCCAGTCTTCCCTCTTCAGAACTATCCGAGAGAGCTCCGAAACCACTCT 1968  
QY 461 AspLysGluGluAlaSerIleProLysLeuGlnThrAlaArgProSerAspSerGln 480  
DB 1969 GATTAAGAGAGAACCCAGCATCCCAAGAGCTCAGACCGCCAGGCTTCAGACACCAG 2028  
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500  
DB 2029 AGCAGGATGTGATTCGGTCAGAACCCAGAGAGGAGGACCCGCCCAAGAGTCCCTTTA 2088  
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrrHisThrSerPheLeuPheGly 520  
DB 2089 TCTCCATGCTATGAAAGTGGAGGCGTGGAGAGCAATTAACACACAGCTTCCCTTTCGGC 2148  
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLysGlyTyrrPheHis 540  
DB 2149 CTTTCCACCGCCAGACAGACCTCAGAAATGCTGCGCTGGGCTTTAAGGCTGCGCAC 2208  
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrrPheAla 560  
DB 2209 TCGGATATCTTGGCCCCCAGACCTTACCTTCCCTGACAGAGCTGTGATTTTGGC 2268  
QY 561 ThrGluSerSerHisPheTyrrSerAlaSerAlaIleTyrrGlySerAlaSerTyrrSer 580  
DB 2269 ACAGAGTCTCAACACTTACTCTGCTCAGGCATCTTACGAGGCGAGTCCAGTTACTCT 2328  
QY 581 AlaTyrrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrrSerValArgArg 600  
DB 2329 GCTTACAGCTGACGCGCAGCTGCCACTTGCAGGACCAAGTCAATTTCTGTGGCAGG 2388  
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrrHisGluGlnSerProPheGln 620  
DB 2389 CAGAAACCAAGTACAGAGACTGATCGCGCGAGCTGGCAATGAAGAGCCCTTTGAA 2448  
QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAsn 640  
DB 2449 AAGCAGATTAAACGAGAACTGCCAAATGGAATTTGAGAGACATCATGTCAAGAGAAC 2508  
QY 641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660  
DB 2509 AGGTACCGGAAAGAGCTGGGAAAGTGGGCAATGATTAAGCTTTTTCGGGCGACATGGA 2568  
QY 661 IleIleGluValSer 665  
DB 2569 ATCATTTAGAGTCTCC 2583

RESULT 5  
ABV26923  
ID ABV26923 standard; cDNA; 5145 BP.  
XX  
AC ABV26923;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 26914.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX pharmacodynamic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US005171.  
XX  
PR 17-FEB-2000; 2000US-018319P.  
XX 16-MAR-2000; 2000US-0189862P.  
XX 25-MAY-2000; 2000US-0207454P.  
XX 09-JUN-2000; 2000US-0211314P.  
XX 18-JUL-2000; 2000US-0219007P.  
XX 13-DEC-2000; 2000US-0255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
XX WPI; 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.  
XX  
PS Claim 1; Page 5449-5450; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX  
XX Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;  
SQ  
Alignment Scores:  
Pred. No.: 0 Length: 5145  
Score: 3406.00 Matches: 663  
Percent Similarity: 99.85% Conservative: 1  
Best Local Similarity: 99.70% Mismatches: 1  
Query Match: 99.65% Indels: 0  
DB: 1 Gaps: 0  
US-10-029-345A-109 (1-665) x ABV26923 (1-5145)  
QY 1 MetAlaHisGluNecIleGlyThrGluIleValThrGluArgLeuValAlaLeuLeuGlu 20  
DB 589 ATGGCCCATGAGATGATTGGAACCAATTTGTTACTGAGAGGTGGCTGCTGCTGGA 648  
QY 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40  
DB 649 AGTGAACGGAAGAAAGTGTCTAATTGATTGACCGGCAATTGTGGAAATCAATACATCC 708

QY 41 HisIleLeuGluAlaIleAsnIleAsnCySerLyLeuMetLyArgArgLeuGluGln 60  
DB 709 CACATTTTGGAGCCATTATATCACTCTCCAACTTATGAAAGGAGGTTGCAACAG 768  
QY 61 AspLyValLeuIleThrGluLeuIleGlnHisSerAlaValHisLyValAspIleAsp 80  
DB 769 GACAAAGTGTATTAACAAGCTCATCCAGCATTCGCGAAMATAGTTGACATTGAT 828  
QY 81 CysSerGlnLyValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100  
DB 829 TGCAGTCAGAGGTTGTAGTTTTCGATCAAGAGCTCCCAAGATTTGCTTCTCTTCA 888  
QY 101 AspCyPheLeuThrValLeuLeuGlyLySLeuGlyLySerPheAsnSerValHisLeu 120  
DB 889 GACTGTTTCTGACTGTTACTTCTGGGTAACTGAGAAAGAGCTTCAACTCTGTCACTG 948  
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCyPheProGlyLeuCySerGlyGlyLySer 140  
DB 949 CTTCAGAGTGGGTTTCTGAGTTCTCTGTTGTTTCCCTGCGCTCTGTGAGAAATCC 1008  
QY 141 ThrLeuValProThrCysHisSerGlnProCySLeuProValAlaAsnIleGlyProThr 160  
DB 1009 ACTCTAGTCCCTAAGCTGCAATTTCTCAGCTTGTCTTACCTGTTGCCAATGAGCCAAAC 1068  
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCySLeuArgAspValLeuAsnLySLeuLeu 180  
DB 1069 CGAATTCCTCCCAATTTTATCTTGCTGCTGCGAGAGATGCTCTCAACAAGAGCTGATG 1128  
QY 181 GlnGlnAsnGlyTleGlyTyrValLeuAsnAlaSerTyrThrCysProLyProAspPhe 200  
DB 1129 CAGCAAGATGGAGTGTATGTATGTTAAATGCAGCAATACCTGTCAAAAGCTGACTTT 1188  
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCySerGlyValIleLeu 220  
DB 1189 ATCCCGAGTCTATTTCTGCGTGTGCTGTAAGAGAGCTTTGTGAAATTTTG 1248  
QY 221 ProTyrLeuAspLySerValAspPheIleGluLyAlaValAsnAsnGlyCyVal 240  
DB 1249 CGGTGTTGGACAATCAGTAGATTTCATTGAGAAAGCAAAAGCCCTCAATGATGTGT 1308  
QY 241 LeuValHisCysLeuAlaGlyTleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260  
DB 1309 CTAGTCACTGTTTACTGAGATCTCCCTCGCCAGCAATCCCTATCCGCTACATCATG 1368  
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluLySAspProThr 280  
DB 1369 AAGAGGATGACATGCTTTAGATGAGCTTACAGATTGTGAAAGAAAAAAGACCTACT 1428  
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlyLySValIleLyAsn 300  
DB 1429 ATATCTCCAACTTCAATTTTCTGGGCCCAATCTTGACCTAGAGAAAGATTAAAGAC 1488  
QY 301 GlnThrGlyAlaSerGlyProLySerLySLeuLyLeuLeuHisLeuGlyLyProAsn 320  
DB 1489 CAGACTGAGACATCAGAGGCCAAAGACCAATCAACTGCTGCACTGAGAGCCAAAT 1548  
QY 321 GluProValProAlaValSerGluGlyGlnLySValIleThrProLeuSerProPro 340  
DB 1549 GAACCTGCTCCCTGCTGTCTCAGAGGTTGACAGAAAGAGAGCGCCCTCACTCAACC 1608  
QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360  
DB 1609 TGTGCCGACTCTCTCACTCAGAGGACAGACAGCAAGAGCCCTGATCCGCGCACTG 1668  
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380  
DB 1669 CCCAGCGTCCCAAGCTGACAGCGGTGCTGTGTTAGAGAGACAGCCGCTGTATCAGCGCTC 1728  
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLySValIleLySAspSerPhe 400  
DB 1729 AGTGGCTGACCTGTCCGACAGCAGGCTGAGAGACAGCAATAGCTCAAGCCTTCTTC 1788  
QY 401 SerLeuAspIleLySerValSerTyrSerAlaSerMetAlaIleSerLeuHisGlyPhe 420



Db 949 CTTCAGAGTGAGTTGCTGAGTTCTCTGTTGTTCCCTGCGCTCTGAGGAAAATCC 1008  
 Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAenIleGlyProThr 160  
 Db 1009 AGCTACATCCCTACCTCAATTTCTCAGCCTTGCTTACCTGTGCAACATGGGCAACC 1068  
 Qy 161 ArgIleLeuProAenLeuTyrLeuGlyCysGlnArgAspValLeuAenIleGlyLeu 180  
 Db 1069 CGAATCTTCCCAATCTTTATCTTGCTGCTGCAGGAGATGTCCTCAACAAAGAGCTGATG 1128  
 Qy 181 GlnGlnAenGlyIleGlyTyrValLeuAenAlaSerTyrThrCysProIleProAspPhe 200  
 Db 1129 CACAGATGAGATGGATTGCTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 1188  
 Qy 201 ILProGlnSerHisPheLeuArgValProValAspAspSerPheCysGlyValIleLeu 220  
 Db 1189 ATCCCCAGATCTCAATTCCTGCGTGCTGTGATACAGACTTGTGTGAAAAATTTTG 1248  
 Qy 221 ProTyrLeuAspIleSerValAspPheIleGlyValAlaIleValAlaSerAenGlyCysVal 240  
 Db 1249 CCGTGGTTGGACAATACAGTNGATTTCAATTGAGAAACAAAGCCTCCATGATGCTT 1308  
 Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260  
 Db 1309 CTAGTGCACTGTTAGCTGGGATCTCCGCTCCGCCACATCGCTATCGCTACATCATG 1368  
 Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGlyValAspArgProThr 280  
 Db 1369 AAGAGATGAGACATGCTTTAGATGAAGCTTACAGATTGTGAAAGAAAAGAAAGCACTACT 1428  
 Qy 281 ILSerProAenPheAenPheLeuGlyGlnLeuLeuAspTyrGlyValIleValAsn 300  
 Db 1429 ATATCTCCAACTTCAATTTTCTGGGCCATCTCTGACATATGAGAAAGATTAAAGAAC 1488  
 Qy 301 GlnThrGlyAlaSerGlyProIleSerTyrLeuLeuIleLeuHisLeuGlnIleValProAsn 320  
 Db 1489 CAGACTGAGACATCAGGGCCAAAGAGCAAACTCAAGCTGTGACCTGGAGAAAGCCAAAT 1548  
 Qy 321 GluProValProIleValIleSerGlnGlyGlnIleSerGlnIleProIleSerProPro 340  
 Db 1549 GAACCTGTCTCTGCTGCTCAGAGGAGTGAGACAGAAAAGCAAGAGCCCTCAGTCCAGCC 1608  
 Qy 341 CysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHisProAlaSerVal 360  
 Db 1609 TGTGCCGACTCTCTACTCAGAGGCAAGCAAGCAAAAGCCCTGCTGATCCCGCAGGCTG 1668  
 Qy 361 ProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAlaLeu 380  
 Db 1669 CCCAGCGTCCAGCGTGCAGCCGCTGCTGTAGAGGACAGCCGCTGTATACAGGCGCTC 1728  
 Qy 381 SerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerHisLeuValAspSerPhe 400  
 Db 1729 AGTGGGCTGACCTGTCCGAGACAGGCTGAAAGACGCAATAGCTCAAGCGTTCCTTC 1788  
 Qy 401 SerLeuAspIleLeuSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420  
 Db 1789 TCTCTGATATCAAAATAGTTTCAATATTCAGCCAGCATGCGACATCTTACATGCTTC 1848  
 Qy 421 SerSerSerGlnAspAlaLeuGlnTyrTyrIleAspSerThrThrLeuAspGlyThrAsn 440  
 Db 1849 TCTCTCATCAAGAAAGTCTTGGAAATACCAAACTTCCACTACTCTGATGGGACCAAC 1908  
 Qy 441 LysLeuCysGlnPheSerProValGlnGlnLeuSerGlnIleHisProGlnIleThrSerPro 460  
 Db 1909 AAGCTATGCGAGTCTCCCTGTTCAAGAACTATCGAGAGCACTCCCGAAACCAAGCTCT 1968  
 Qy 461 AspLysGlnGlnAlaSerIleProIleValLeuGlnIleThrAlaArgProSerAspSerGln 480  
 Db 1969 GATTAAGAGAGAAAGCAATCTCCCAAGAACTGAGAGCCCGCAGCCTTACAGACGACAG 2028  
 Qy 481 SerIleArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500  
 Db 2029 AGCAAGCGATTGATCGGTCAAGAACAGAGCAGTGGCAGCCGCGCAGAGTCCCTTTTA 2088

Qy 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520  
 Db 2089 TCTCCATCTGATGAAGTGGAGCTGAGAGCAATTAACACCAAGCTTCTTTCCGCG 2148  
 Qy 521 LeuSerThrSerGlnGlnHisLeuThrIleValSerAlaGlyLeuGlyLeuValGlyTyrHis 540  
 Db 2149 CTTTCCAGCAGCCAGCAGCACTCACAGAGTGTGTGCTGGCGCTTAAGGCTGGCAC 2208  
 Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560  
 Db 2209 TCGATATCTTGCCCCCCCCAGACCTTACCTCCCTGACCGACGCTGTATTTTGCC 2268  
 Qy 561 ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyIleSerAlaSerTyrSer 580  
 Db 2269 ACAAGTCTCTCACTTACTTCTGCTCAGCCATTCAGAGGCAATGCTCACTTACTCT 2328  
 Qy 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600  
 Db 2329 GCCTACAGCTGACGACGAGCTGCCACTTGCGAGACCAAGTCTATCTGTGCGCAGCGG 2388  
 Qy 601 GlnIleProSerAspArgAlaAspSerArgArgSerTyrHisGlyGlnIleSerProPheGlu 620  
 Db 2389 CAGAACCAAGTACAGAGCTGACTCGCGCGAGCTGGCATGAAAGAGACCCCTTTGAA 2448  
 Qy 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSerIleMetSerGluAsn 640  
 Db 2449 AAGCATTTTAAACGCAAGAGCTCCAAATGGAATTTGAGAGAGCATCATCTCAGAGAAC 2508  
 Qy 641 ArgSerArgGlnGlnLeuGlyIleValGlySerGlnSerSerPheSerGlySerMetGlu 660  
 Db 2509 AGGTCACGGGAAGAGCTGGGGAAGTGGGAGTCAAGTCACTTTCCGSCACATGGA 2568  
 Qy 661 IleIleGluValSer 665  
 Db 2569 ATCATTAAGGTCTCC 2583

RESULT 7  
 ABV28657 standard; cDNA; 5145 BP.  
 ABV28657;  
 AC XX  
 DT 16-SEP-2002 (first entry)  
 XX XX  
 DE Human prostate expression marker cDNA 28648.  
 XX XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynanamic marker;  
 KM pharmacogenomic marker; gene; ss.  
 XX XX  
 OS Homo sapiens.  
 XX XX  
 PN W0200160860-A2.  
 XX XX  
 PD 23-AUG-2001.  
 XX XX  
 PF 20-FEB-2001; 2001MO-US005171.  
 XX XX  
 PR 17-FEB-2000; 2000US-018319P.  
 PR 16-MAR-2000; 2000US-0189862P.  
 PR 09-MAY-2000; 2000US-0207454P.  
 PR 09-JUN-2000; 2000US-0211314P.  
 PR 18-JUL-2000; 2000US-0219007P.  
 PR 13-DEC-2000; 2000US-0255281P.  
 XX XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX XX  
 PI Schlegel R, Endege WO, Monahan JB;  
 XX XX  
 DR WPI, 2001-662795/76.  
 XX XX  
 PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer.  
XX Claim 1; Page 6009-6010; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (1) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV6213) of the  
CC specification or its complement. (1) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or incidence of prostate cancer in a patient  
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX

SQ Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

## Alignment Scores:

Pred. No.:	0	Length:	5145
Score:	3406.00	Matches:	663
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.70%	Mismatches:	1
Query Match:	99.65%	Indels:	0
DB:	1	Gaps:	0

US-10-029-345A-109 (1-665) x ABV28657 (1-5145)

QY 1 MetAlaHISGLuMeTILEGlyThrGlnTLeValThrGluArgLeuValAlaLeuLeuGlu 20  
DB 569 ATGGCCCATGAGATATGGAATCTAAATTTGACTGAGAGGTGGTGGCTCTGCTGGAA 648  
QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40  
DB 649 AGTGAAGGAAAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 708  
QY 41 HistLeuGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60  
DB 709 CACATTTTGGAAAGCCATTATATCAACATGCTCAAGCTTATGAAAGCGAAAGCTTCAACAG 768  
QY 61 AspLysValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80  
DB 769 GACAAAGGTTTATATACAGAGCTATCCAGCATTCAGGAAACATTAAGTTGACATTTGAT 828  
QY 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100  
DB 829 TGCAGTCAGAGAGTTGTGATTTAGATCAAAAGCTCCCAAGATGTGGCTCTCTCTTCA 888  
QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGlyLysSerPheAsnSerValHisLeu 120  
DB 889 GACTGTTTCTCAGCTGATCTTCTGGGTAACTGGAGAAAGACCTTCACTGTTCACCTG 948  
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyLysSer 140  
DB 949 CTTCAGAGTGGGTTTGTGAGATTTCTCTGCTTTCCCTGGCCCTCTGTGAAGAAATTC 1008  
QY 141 ThrLeuValProThrCysHisSerGlnProCysLeuProValAlaAsnIleGlyProThr 160  
DB 1009 ACTCTAGTCCCTACCTGATTTCTCAGCTTCTTACCTGTTCACCATTTGGGCCAAC 1068  
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180  
DB 1069 CGAATTTCTCCAACTTATCTTGGCTGCGCAGGAGATGTCTTCAACAAAGAGCTGATG 1128  
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200  
DB 1129 CAGCAGATGGAGTTGGTTAGTTAAATCCAGCATACCTCTCCAAAGCCGATTTT 1188  
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlyLysIleLeu 220  
DB 1189 ATCCCGAGTCTCATTTCTGCTGTGCTGTGAATGACAGCTTTTGTGAAGAAATTTTG 1248

QY 221 ProThrLeuAspLysSerValAspPheIleGluLysValAlaLysAsnGlyCysVal 240  
DB 1249 CCGTGGTTGGACAAATGATGATTTTATGAGAAACAAAGCTTCAATGATGTGTT 1308  
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260  
DB 1309 CTATGTCACCTGTTTATAGCTGGGATCTCCGCTCCGCCACCATCGGTATCGCTCATCATG 1268  
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrThrPheValLysGlyLysArgProThr 280  
DB 1369 AAGAGATGACATGCTTTTATGATGAGCTTACAGATTTGTGAAGAAAGAAACCTACT 1428  
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlnLysLysIleLysAsn 300  
DB 1429 ATATCTCCAAACTTCAATTTTCTGGCCCACTCTGGACATATGAGAAAGATTTAAGAC 1488  
QY 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlyLysProAsn 320  
DB 1489 CAGACTGAGCATCAGGCGCAAGAGCAACTCAAGCTGCTGCACCTGGAGAGCCAAAT 1548  
QY 321 GluProValProAlaValSerGlyGlyGlnLysSerGluThrProLeuSerProPro 340  
DB 1549 GAACCTGCTCCCTGCTGTCTAGAGGTGACAGAAAAAGCAGACGCCCTCAGTCCACCC 1608  
QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360  
DB 1609 TGTGCCAGCTCTGCTACTCTCAGAGGACAGAGCAAAAGCCGCTGATCCCGCACCGTG 1668  
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380  
DB 1669 CCGAGCGTCCCGCAGCGCTGACCGCTGTGATGAGAGACAGCCGCTGTACAGGGGCTC 1728  
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLysArgSerPhe 400  
DB 1729 AGTGGCTGACCTGCTCCGACAGAGCTGGAGAGCAATAGCTTCAAGGCTTCTTC 1788  
QY 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420  
DB 1789 TCTCTGATATCAATCAATGATTTTCAATTCAGGCAGATGAGCATCTTATACGCTTC 1848  
QY 421 SerSerSerGlnAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440  
DB 1849 TCTCTCATGAAAGATCTTTGAAATCTAACAACTTCCATCACTCTGATGGAGCAAC 1908  
QY 441 LysLeuCysGlnPheSerProValGlnGlyLeuSerGlnGlyThrProGlnThrSerPro 460  
DB 1909 AAGCTATGCCAGTCTCCCTGTTCAAGAACTATGAGAGCAACTCCCAAAACGATCCT 1968  
QY 461 AspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480  
DB 1969 GATTAAGAGAAAGCCAGCATCCCAAGAAAGCTGACAGCCGACGCTTCAACAGCCAG 2028  
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500  
DB 2029 AGCAAGCATTTGATTTGGGTGACAAACAGACAGAGGAGCCGACAGAGGCTCTTTTA 2088  
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520  
DB 2089 TCTCCAGCTCATCGAAGTGGAGCGGTGAGAGCAATTTACACACAGCTCTCTTTTGGCC 2148  
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540  
DB 2149 CTTTCCACAGCAGCAGACACCTCCAGAACTGTGCTGGCTGGGCTTAAAGGGCTGGCAC 2208  
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerThrPyrPheAla 560  
DB 2209 TCGGATATTTGGCCCCCAGACCTTACCTCTCTGACAGAGAGCTGGATTTTGGCC 2268  
QY 561 ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer 580  
DB 2269 ACAGAGTCTTCACTTGTACTGCTCTCAGCAGCATCTAGAGGAGAGGACGATTAAGCTT 2328  
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600

Db 2329 GCCTACAGCTGACGCCAGCTGCTCCACTTGGCGAGACCAAGTATCTGTGCCAGCGG 2388  
QY 601 GlnlyProSerPepaAlaAspSerArgArgSerTrpIleGluGluSerProPheGlu 620  
Db 2389 CAGAACGCAAGTACAGAGCTGACTCGCGGAGCTGCGATAGAAAGACCCCTTTGAA 2448  
QY 621 LysGlnPheIleArgArgSerCysGlnMetGluPheGluGluSerIleMetSerGluAsn 640  
Db 2449 AACGAGTTTAAACGACAGACCTGCCAATGGAATTTGAGAGACATCATCTCAGAGAAC 2508  
QY 641 ArgSerArgGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 660  
Db 2509 AGGTCAAGGAGAAAGCTGGGAAAGTGGGACATGCTAGCTTTTGGGACAGATGAA 2568  
QY 661 IleIleGluValSer 665  
Db 2569 ATCATTGAGGCTCC 2583  
RESULT 8  
ABV22827  
ID ABV22827 standard; cDNA; 5145 BP.  
AC ABV22827;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 22818.  
XX  
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX pharmacogenomic marker; gene; ss.  
XX Homo sapiens.  
XX MO200160860-A2.  
XX  
XX 23-AUG-2001.  
XX  
XX 20-FEB-2001; 2001MO-US005171.  
XX  
XX 17-FEB-2000; 2000US-0183319P.  
XX 16-MAR-2000; 2000US-0189862P.  
XX 25-MAY-2000; 2000US-0207454P.  
XX 09-JUN-2000; 2000US-0211314P.  
XX 18-JUL-2000; 2000US-0219007P.  
XX 13-DEC-2000; 2000US-0255281P.  
XX  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
XX Schlegel R, Endege WO, Monahan JE;  
XX  
XX WPI; 2001-662795/76.  
XX  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
XX prostate cells and correlating with presence of prostate cancer, useful  
XX for detecting presence of prostate cancer, stage of prostate cancer.  
XX  
XX Claim 1; Page 4033-4034; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
XX specification or its complement. (I) is useful for: (a) assessing whether  
XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy  
XX of a test compound to inhibit prostate cancer in a patient; (c) assessing  
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;  
XX (d) selecting a composition for inhibiting prostate cancer in a patient;  
XX (e) assessing the prostate cell carcinogenic potential of a compound; (f)  
XX determining whether prostate cancer has metastasized in a patient; (g)  
XX assessing the aggressiveness or indolence of prostate cancer in a patient  
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX  
XX Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;

Alignment Scores:  
Pred. No.: 0 Length: 5145  
Score: 3406.00 Matches: 663  
Percent Similarity: 99.85% Conservative: 1  
Best Local Similarity: 99.70% Mismatches: 1  
Query Match: 99.65% Indels: 0  
Gaps: 0  
US-10-029-345A-109 (1-665) x ABV22827 (1-5145)  
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuGlu 20  
Db 589 ATGGCCCATGAGATGATGATTGGAATCAATTTGTTACTGAGAGGTTGGCTGCTGAGAA 648  
QY 21 SerGlyThrGluLysValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40  
Db 649 AGTGAACGGMAAAGTGTGCTGTAATTTGATGACCGGCCATTGTGTGMAATCAATTAATCC 708  
QY 41 HisIleGluGluAlaIleAsnIleAsnCysSerLysLeuMetLysArgArgLeuGln 60  
Db 709 CACATTTGGAAACCTTATATATCACTGCTCCAGCTTATGAAAGGAGTTGCCAAG 768  
QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80  
Db 769 GACAAAGTTTATATACAGAGCTCATCCAGCATTCAGCGAAACATAGTTGACATTGAT 828  
QY 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAspSerLeuSerSer 100  
Db 829 TGCAGTCAGAAAGTTTATGTTTACGATCAAAAGCTCCCAAGATTTGCTCTCTCTTCA 888  
QY 101 AspCysPheLeuThrValLeuLeuGluLysLysGluLysSerPheAsnSerValHisLeu 120  
Db 889 GACTGTTTCTACTGTTACTTCTGGGTAACTGGAAGAAGCTTCACTCTGTTCACTG 948  
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGluGlyLysSer 140  
Db 949 CTTCGAGAGTGGGTTTCTGAGTTCTCTCGTTGTTTCCCTGCGCTGTGMAAGAAATCC 1008  
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160  
Db 1009 ACTCTAGTCTCTACCTGACATTTCTCAGCCTGTCTTACCTGTTCACAAATGGGCCAAC 1068  
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180  
Db 1069 CGAATTTCTCCAAATCTTATCTTGTGCTGCGACGAGATGCTCTCAACAGAGGCTGATG 1128  
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200  
Db 1129 CAGCAGATGAGATTTGTTATGTGTTAAATCCAGCAATACCTGTCCAAAGCTGACTTT 1188  
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220  
Db 1189 ATCCCGAGTCTCATTTCTGCGCTGTGCTGTGAAGACAGCTTTGTGAGAAATTTTG 1248  
QY 221 ProThrLeuAspLysSerValAspPheIleGluValAlaLysAsnGlyCysVal 240  
Db 1249 CCGTGTGTGACAAATCAGTATTCATTTGAAAGACAAACCTCCCAATGATGTTGTT 1308  
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260  
Db 1309 CTATGTCACGTGTTTACTGAGGATCTCCGCTCGGCACACATGCTATCGCTACATCAG 1368  
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysValArgProThr 280  
Db 1369 AAGAGATGACATGCTTCTTATGATGAAAGCTTACAGATTTGTGMAAAGAAACACTACT 1428  
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlyLysLysIleLysAsn 300  
Db 1429 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCTTGACATATGAGAAAGATTAAGAAC 1488  
QY 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGluLysProAsn 320

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Db      1489 CAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGCTCAGCTGAGAGAGCAAAAT 1548
Qy      321 GIUProValProAlaValSerGluGlyGlnIleuSerGluThrProLeuSerProPro 340
Db      1549 GAACCTGTCTCTGCTCTCTCAGAGGTTGACAGAGAAAGGAGACCGCTTCAGTCCACACC 1608
Qy      341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360
Db      1609 TGTGCGCACTGTCTACCTCAGAGGCGAGAGCAAAAGGCGCTGCATCCGCGCAGCGTG 1668
Qy      361 ProSerValProSerValGlnProSerLeuGluAspSerProLeuValGlnAlaLeu 380
Db      1669 CCCAGGCTCCAGAGCTGAGCGCTGTGTAGAGAGACGCCCTGCTACAGGCGCTC 1728
Qy      381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAlaLeuValSerGlyArgSerPhe 400
Db      1729 AGTGGGCTGTGACCTGTGCGCAGAGGCTGAGAGACAGAAATACCTCAGGTTCTTC 1788
Qy      401 SerLeuAspIleLeuSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
Db      1789 TCTCTGGATATCAAAATCAGTTTCATATTCAGCCAGCATGCGCATCTTACATGGCTTC 1848
Qy      421 SerSerSerGluAspAlaLeuGlnIleuTyrTyrProSerThrThrLeuAspGlyThrAsn 440
Db      1849 TCTCATCAGAGAGATGCTTTGGAAATACCAAACTTCACACTCTGTGATGGAGCCAC 1908
Qy      441 LysLeuCysGlnPheSerProValGlnIleuSerGluGlnThrProGluThrSerPro 460
Db      1909 AAGCATATGCGAGTCTCCCTGTTTCCAGAACTATGAGAGACGCTCCGAAACAGTCTCT 1968
Qy      461 AspLysGluGluAlaSerIleProLysLeuGlnThrAlaArgProSerAspSerGln 480
Db      1969 GATTAAGAGAGAAAGCAGATCCCAAGAGCTGAGACCGCCAGGCTTTCAGACAGCCAG 2028
Qy      481 SerLysAspGluHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db      2029 AGCAAGCATATTCATTCGCTGAGAACCAAGCAGCAGTGGCAGCCCGCAGAGTCCCTTTA 2088
Qy      501 SerProLeuHisArgSerGlySerValGlnAspPheTyrHisSerPheLeuPheGly 520
Db      2089 TCTCCACATCGAATCGAAGTGGAGCGTGGAGAGCAATATCCACACAGCTTCTTTGGGC 2148
Qy      521 LeuSerThrSerGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540
Db      2149 CTTTCACAGCAGCAGCAGCAGCTTCAGAAAGTCTGTGCTGGCTTAAAGGCTGCGCAC 2208
Qy      541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
Db      2209 TCGATATCTTGGCCCCCAGACCTTACCCCTTCCTGACACAGCAGCTGTATTGGCC 2268
Qy      561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer 580
Db      2269 ACAGAGTCTTCACTTCTACTGCTGCTCAGCCATCTACGAGGACAGGACAGTACTCT 2328
Qy      581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
Db      2329 GCTTACAGCTCAGCAGCTGCCCACTTGCAGAAACCAAGCTATCTGTGCGCAGGCGG 2388
Qy      601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGluGlnIleuSerProPheGlu 620
Db      2389 CAGAAAGCCAAAGTGAAGAGTGAAGTCTGCGGCGAGGCTGGCATGAAGAGAGCCCTTTGAA 2448
Qy      621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSerIleMetSerGluAsn 640
Db      2449 AAGCAGTTTAAACCAAGAGCTGCCAAATGGAATTTGGAGAGCATCATGTCCAGAGAAC 2508
Qy      641 ArgSerArgGluGluLeuGlyLeuValGlySerGlnSerPheSerGlySerMetGlu 660
Db      2509 AGGTCAAGGAGAGAGCTGGGAAAGTGGGCACTACATGCTTCTTGGGAGAGCATGAA 2568
Qy      661 IleIleGluValSer 665
Db      2569 ATCATGAGGCTCTCC 2583

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RESULT 9
ABV26934
ID      ABV26934 standard; cDNA; 5145 BP.
XX
AC      ABV26934;
XX
DT      16-SEP-2002 (first entry)
XX
DE      Human prostate expression marker cDNA 26925.
XX
KW      Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX      pharmacogenomic marker; gene; ss.
XX
OS      Homo sapiens.
XX
W020160860-A2.
XX
PN      23-AUG-2001.
XX
PD      20-FEB-2001; 2001WO-US005171.
XX
PF      17-FEB-2000; 2000US-0183319P.
XX
PR      16-MAR-2000; 2000US-0189662P.
XX
PR      25-MAY-2000; 2000US-0207454P.
XX
PR      09-JUN-2000; 2000US-0211314P.
XX
PR      18-JUL-2000; 2000US-0219007P.
XX
PR      13-DEC-2000; 2000US-0255281P.
XX
PA      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI      Schlegel R, Endege WO, Monahan JE;
XX
DR      WPI; 2001-662795/76.
XX
PT      Novel isolated nucleic acid molecule associated with cancerous state of
PT      prostate cells and correlating with presence of prostate cancer, useful
PT      for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS      Claim 1; Page 5453-5454; 11750pp; English.
XX
XX
CC      The invention relates to an isolated nucleic acid molecule (1) comprising
CC      a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC      specification or its complement. (1) is useful for: (a) assessing whether
CC      a patient is afflicted with prostate cancer; (b) monitoring the
CC      progression of prostate cancer in a patient; (c) assessing the efficacy
CC      of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC      the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC      (e) selecting a composition for inhibiting prostate cancer in a patient;
CC      (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC      determining whether prostate cancer has metastasized in a patient; (h)
CC      assessing the aggressiveness or indolence of prostate cancer in a patient
CC      ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ      Sequence 5145 BP; 1408 A; 1135 C; 1253 G; 1346 T; 0 U; 3 Other;
XX
XX
Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 1 Gaps: 0
US-10-029-345A-109 (1-665) x ABV26934 (1-5145)
Qy      1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db      589 ATGGCCCATGAGATGATGGAACTCAAAATTTGTTACTGAGAGGCTTGCTGCTGCGAA 648
Qy      21 SerGlyThrGluLysValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
Db      649 AGTGAACGAGAAAGAGTCTGCTAATTATTAATACCGCGCATTTTGTGAATACATATCATCC 708

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QY 41 HisIleuGluAlaIleAsnIleAsnCySerIysLeuMetLysArgArgLeuGln 60  
 DB 709 CACATTTGGAAAGCATTAATATCACTGCTCCAAAGCTTATGAAGCAAGTTGCACAG 768  
 QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80  
 DB 769 GACAAAGTGTAAATTACAGAGCTCATCAGCATTCACAGAAACATAAGTTGACATTGAT 828  
 QY 81 CySerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100  
 DB 829 TGCAGTCAGAGGTTGATGTTAGATCAAGCTCCCAAGATGTGCTCTCTCTTCA 888  
 QY 101 AspCySerPheLeuThrValIleLeuGluLysLeuGluLysSerPheAsnSerValHisLeu 120  
 DB 889 GACTGTTTCTCACTGACTGACTTCTGGTAACTGGAGAAAGACTTCACACTGTTCACTG 948  
 QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCySerPheProGlyLeuCySerGluGlyLysSer 140  
 DB 949 CTTCAGAGTGGGTTGCTGAGATTCTCGTTGTTTCCCTGGCCCTCTGTAAGGAAATCC 1008  
 QY 141 ThrLeuValProThrCysIleSerGlnProCySerLeuProValAlaAsnIleGlyProThr 160  
 DB 1009 ACTCTAGTCCCTACCTGCAATTTCTCAGCCCTTGCTTACCTGTGCACATTGGGCCAAC 1068  
 QY 161 ArgIleLeuProAsnLeuTyrLeuGluCySerGluArgAspValLeuAsnLysGluLeuIle 180  
 DB 1069 CGAATTTCTCCCAATCTTTATCTTGCTGCCAGGAGAAATGCTCCCAACAAAGAGCTATG 1128  
 QY 181 GlnGluAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200  
 DB 1129 CAGAGAAATGGGATTTGTTATGTGTAAATGCCAGCAATACCTGTCCAAAGCCGACTTT 1188  
 QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCySerGluLysIleLeu 220  
 DB 1189 ATCCCCAGTCTCAATTCCTGCGGTGCTCGTGAATACAGCTTTTGTGAATAATTTTG 1248  
 QY 221 ProThrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240  
 DB 1249 CCGTGTGGAGCAAAATGATGATTTCAATTGAAAGCAAAAGCTCCAAATGATGTGTT 1308  
 QY 241 LeuValHisCySerLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260  
 DB 1309 CTAGTGCACTGTTAGCTGGGATCTCCGCTCCGCCCACTCGCTATCGCTATCATCATG 1368  
 QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProThr 280  
 DB 1369 AAGAGATGACATGCTTTAGATGAAGCTTACGATTTGTGAAGAAAAAGACTTACT 1428  
 QY 281 IleSerProAsnPheAsnPheLeuGluLysLeuLeuAspTyrGluLysLysIleLysAsn 300  
 DB 1429 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCTGCACTATGAGAAAGATTAAAC 1488  
 QY 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLysIleLeuGluLysProAsn 320  
 DB 1489 CAGACTGGAGCATCAGGGCCAAAGCAAACTCAAGCTGTGACCTCGAAGAACCAAT 1548  
 QY 321 GluProValProAlaValIleSerGluGlyGluLysSerGluThrProLeuSerProPro 340  
 DB 1549 GAACCTGTCTCTGCTGCTCAGAGGTGACAGAAAAAGCAAGAGCCCTCAGTCCACCC 1608  
 QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGluArgProValHisProAlaSerVal 360  
 DB 1609 TGTGCCACTCTGCTACTCAGAGGCAAGCAAGCAAAAGGCCGTGATCCCGCAGGCTG 1668  
 QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380  
 DB 1669 CCCAGCTGCCAGCGTGCAGCCCTCGCTGTAAAGACAGCCGCTGTATCAGGCGCTC 1728  
 QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerLeuLysLeuLysArgSerPhe 400  
 DB 1729 AGTGGCTGACCTGTCCGAGACAGGCTGAAAGACAGCAATAAGCTCAAGCGTTCTTC 1788

QY 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420  
 DB 1789 TCTCTGGATATCAAAATCAGTTTATATATTCAGCCAGATGGCAATCTTACTATGGCTTC 1848  
 QY 421 SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440  
 DB 1849 TCTTCATCAGAAAGATGCTTTGGAAATCTACAAACCTTCCACTCTGATGGAGCAAC 1908  
 QY 441 LysLeuCySerGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460  
 DB 1909 AAGCTATGCAAGTTCCTCCCTGTTCAAGAACTATCGAGAGACTCCCGAAACCAAGCTC 1968  
 QY 461 AspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480  
 DB 1969 GATTAAGAGAGAACCCAGCATCCCAAGAACTGCACAGCCGACGCTTCAGACAGCAG 2028  
 QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500  
 DB 2029 AGCAGAGATTCATTCGTCAGAACCCAGCAGCAGAGTGGCACCCGCCAGAGTCCCTTTTA 2088  
 QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520  
 DB 2089 TCTTCATGCTGATGAGTGGAGCGTGGAGAGCAATTAACACACAGCTTCTTTTCGGC 2148  
 QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrPhe 540  
 DB 2149 CTTTCCACAGCCAGCAGACACTTCAGAACTCGCTGGCCCTTAAGGCTGGCAC 2208  
 QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560  
 DB 2209 TCGGATATCTTGCCCCCCCCAGACCTTACCCCTTCCCTGCACAGAGCTGTATTTTGGC 2268  
 QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerAlaSerTyrSer 580  
 DB 2269 ACAGAGCTCTCAGACTTACTGCTGCTCAGCCATCAGAGAGCAGTGCAGTACTCT 2328  
 QY 581 AlaTyrSerCySerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600  
 DB 2329 GCCTACAGCTGAGCCAGCTGCCCACTTGGGAGACCAAGTCTATTTCTGCCAGGCG 2388  
 QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSerProPheGlu 620  
 DB 2389 CAGAAACCAAGTACAGAGCTGACTCGCGGAGCTGCGCATAGAGAGACCCCTTGAA 2448  
 QY 621 LysGlnPheLysArgArgSerCySerGlnMetGluPheGlyGluSerIleMetSerGluAsn 640  
 DB 2449 AAGCAGTTTAAAGCAGAAAGCTGCCAAATGGAATTTGGAGAGACATCATGTACAGAAC 2508  
 QY 641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660  
 DB 2509 AGCTCACGGGAAGAGCTGGGGAAGTGGCAGTCACTTCTTTCGGGACACATGGAA 2568  
 QY 661 IleIleGluValSer 665  
 DB 2569 ATCATTGAGGTCCTCC 2583  
 DB  
 RESULT 10  
 ID ADAS3105 standard; cDNA; 2102 BP.  
 ID ADAS3105;  
 AC ADAS3105;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human coding sequence, SEQ ID 673.  
 XX  
 KW Cytotoxic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;  
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;  
 KW inflammatory disease; osteoporosis; neurological disease; gene; ss.  
 OS Homo sapiens.  
 XX  
 PN BP1293569-A2.

XX PD 19-MAR-2003.  
XX PF 21-MAR-2002; 2002EP-00006586.  
XX PR 14-SEP-2001; 2001JP-00328381.  
XX PR 24-JAN-2002; 2002OS-0350435P.  
XX PA (HELI-) HELIX RES INST.  
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Irie R, Tamechika I,  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuko Y;  
DR WPI; 2003-395539/38.  
DR P-PSDB; ADA54744.  
XX  
XX PT New polynucleotides encoding full-length polypeptides, e.g. secretory  
PT and/or membrane proteins, useful for developing medicines for diseases in  
PT which the gene is involved, or as target molecules for gene therapy.  
XX  
XX PS Claim 1; SEQ ID NO 673; 205bp; English.  
XX CC The present invention relates to novel human secretory or membrane  
XX CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-  
XX CC ADA54071). The coding sequences are useful in the gene therapy of  
XX CC diseases caused by abnormalities of the proteins, e.g. cancer,  
XX CC inflammatory diseases, osteoporosis or neurological disease.  
XX SQ Sequence 2102 BP; 542 A; 546 C; 510 G; 504 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 0 Length: 2102  
Score: 3399.00 Matches: 662  
Percent Similarity: 99.70% Conservative: 1  
Best Local Similarity: 99.55% Mismatches: 2  
Query Match: 99.44% Indels: 0  
Gaps: 0  
DB: 1  
  
US-10-029-345A-109 (1-665) x ADA53105 (1-2102)  
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20  
Db 56 ATGGCCCAATGAGATGATTTGAACTCAATTTTACTGAGAGCTTGCGCTCTCTGAAA 115  
QY 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluIleYrAsnThrSer 40  
Db 116 AGTGGAAAGGAAAAAGTCTCTCTAATTGATAGCCGCGCATTTTGGAATACAAATACATCC 175  
QY 41 HisIleLeuGluAlaIleAsnIleAsnGlySerIleuMetIleValArgLeuGlnGln 60  
Db 176 CACATTTTGGAAAGCATTAATATCAACGCTCTCAAGCTTTATGAAGCAAGGTTGCAACAG 235  
QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerAlaValSerHisValAspIleAsp 80  
Db 236 GACAAAGTTTAATTAACAGAGCTCAATCCAGCATTCAGGAAACATTAAGTTGACATTGAT 295  
QY 81 CysSerGlnValValValIleYrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100  
Db 296 TGCAGTCAGAAAGTTGATGATTACATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 355  
QY 101 AspCysPheLeuThrValLeuLeuGlyValLeuGluIleuLysSerPheAsnSerValHisLeu 120  
Db 356 GACGTGTTTCTCACCTGTAATCTTGCTGGTAACTGGAGAAAGAGCTTCAACTCTGTTCACTTG 415  
QY 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuGluGluIleLysSer 140  
Db 416 CTTCAGAGTGGGTTTCTGCTGAGCTTCTCTGTTGTTTCCCTGCGCTCTGTGAAGGAAATCC 475  
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160  
Db 476 ACTCTAGTCCCTACCTGACATTTCTCAGCTTGCTTGAAGCAATTCGAGCAATTCGAGCAAC 535

QY 161 ArgIleLeuProAsnLeuIleuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180  
Db 536 CTAATTTCTCCCAATCTTTAATCTTTGGCTGCCAGGAGATGTCTCAACAAAGAGCTGATG 595  
QY 181 GlnGlnAsnGlyIleGlyIleValLeuAsnAlaSerThrCysProLysProAspPhe 200  
Db 596 CAGCAGAAATGGATGGTATGTTTAAATGCCAGCAATACCTGTCCAAAGCCGTGACTTT 655  
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerThrCysGluValIleLeu 220  
Db 656 ATCCCGAGCTCAATTTCTGCGGTGCTGTAAATGACAGCTTTGTGAAATTTTG 715  
QY 221 ProTrpLeuAspLysSerValAspPheIleGluValAlaValAlaSerAsnGlyCysVal 240  
Db 716 CCGTGTGGACAAATAGTATGATTTTATGAAAGCAAAACCTCCCAATGATGATGTT 775  
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleMet 260  
Db 776 CTAGTGACATGTTTAGCTGGGATCTCCCGCTCCGACCATCTGCTATCGCTACATCATG 835  
QY 261 LysArgMetAspMetSerLeuAspGluAlaIleYrArgPheValLysGluLysArgProThr 280  
Db 836 AAGAGATGACATGCTTTTGAATGAGCTTACAGATTTGTGAAAGAAAGAAAGCACTACT 895  
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTrpGluLysIleLysAsn 300  
Db 896 ATATCTCCAAATCTTCAATTTTCTGGGCCAACTCTGAGCATAGAAAGAAATTAAGAAC 955  
QY 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGluLysProAsn 320  
Db 956 CAGACTGGAGCAATCAGAGGCCAAAGAGCAAACTCAACTGCTGCACTGGAGAAAGCCAAAT 1015  
QY 321 GluProValProAlaValSerGluGlyGlnLysSerGluThrProLeuSerProPro 340  
Db 1016 GAACCTGTCCCTCTCTGTCTCAAGGGTGAACAGAAAGAGAGCGCCCTCACTCACC 1075  
QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360  
Db 1076 TGTGCCAGCTCTCTCACTCAAGAGGACAGGACAAAGGCCGTGATCCCGCAGCGTG 1135  
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380  
Db 1136 CCCAGGTGCCAGCGCTGAGCGCTGCTGTTAAGAGACAGCCCGTGTACAGGGGCTC 1195  
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe 400  
Db 1196 AGTGGCTGCACCTGTCCGACAGACAGCTGGAAGACAGCAATAGCTCAAGCTTCTTC 1255  
QY 401 SerLeuAspIleLysSerValSerTrpSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420  
Db 1256 TCTCTGATATCAATCAATTCATATTCAGCCAGCATGGCAGCATCTTACATGGCTTC 1315  
QY 421 SerSerSerGluAspAlaLeuGluIleuTrpLysProSerThrThrLeuAspGlyLysAsn 440  
Db 1316 TCTCTATCAGAAAGTCTTTGAAATACAAACCTTCCATCTCTGTGATGAGCAAC 1375  
QY 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460  
Db 1376 AAGCTATGCAATCTCTCCCTGTTCAGAAACATATGGAGCAACATCCGAAACAGTCTT 1435  
QY 461 AspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480  
Db 1436 GATTAAGAGAGAGCCAGCATCCCAAGAAAGCTGCAGACTGCAGAGCTTCAACAGCCAG 1495  
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500  
Db 1496 AGCAAGCGATTCATTCGTTGCTCAAGACCAAGCAAGTGGACCGCCCAAGAGTCCCTTTTA 1555  
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTrpHisThrSerPheLeuPheGly 520  
Db 1556 TCTCACTGCAATCGAAGTGGAGGTGGAGGACCAATTCACACCAAGCTTCTTTTCCGCGC 1615

QY 521 LeuSerThrSerGlnGlnIleuThrLysSerAlaGlyLeuGlyLysGlyTyrPheHis 540  
DB 1616 CTTTCCACGACGCGACGACCTTCAGAGATGCTGCTGGCCCTTAAGGGCTGGCAC 1675  
QY 541 SerAspIleLeuAlaProGlnIleThrSerThrProSerLeuThrSerSerTyrPheAla 560  
DB 1676 TCGGATATCTTGGCCCCCGACGACCTTACCCCTTCCCTGACGACGACTGGTATTTTGGCC 1735  
QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer 580  
DB 1736 ACAGAGCTCTCAACCTTCTACTCTGCTTCCACCACTTACGAGAGCGACGACGATCTCT 1795  
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600  
DB 1796 GCGTACAGCTGACGACGCTGCCACCTTGGCGAGAGCCAACTATTTCTGTGGCGAGCGG 1855  
QY 601 GlnLysProSerAspAlaAspSerArgArgSerTyrPheGluGluSerProPheGlu 620  
DB 1856 CAGAGCGCAAGTGCAGAGCTGACTCCGGCGGAGCTGGCATGAGAGACCCCTTTGAA 1915  
QY 621 LysGlnPheLysArgSerCysGlnMetGluPheGlyGlySerIleMetSerGlnAsn 640  
DB 1916 AACGAGTTTAAAGCAGAACGCTGCCAATGAAATTTGAGAGAGCATCATGACAGAAC 1975  
QY 641 ArgSerArgGlnGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660  
DB 1976 AGGTCAACGGGAGAGCGTGGGAAAGTGGGACGTCAGTCTTTCGGGACAGATGGAA 2035  
QY 661 IleIleGluValSer 665  
DB 2036 ATCATTTAGAGTCTCC 2050

## RESULT 11

AAH99685 standard, cDNA; 2966 BP.

16-OCT-2001 (first entry)

Human proteoin encoding cDNA sequence SEQ ID NO:520.

Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
antibacterial; endocrine; cardiant; central nervous system; virucide;  
anti-HIV; fungicide; antinutrient; cardiovascular; anaemic; anaemia;  
antileptegant; haemostatic; vulnery; antitumor; osteopathic; eczema;  
dermatological; antiallergic; antidiabetic; cyclostatic;  
neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
immunostimulant; gene therapy; antilease therapy; vaccine; inflammation;  
antiinflammatory; rheumatoid arthritis; septic shock; pancreatitis;  
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
genetic disease; haematopoietic disorder; platelet disorder; asthma;  
chromocytoma; osteoporosis; severe combined immunodeficiency;  
allergic rhinitis; diabetes; multiple sclerosis; depression;  
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
neurological disorder; ss.

Homo sapiens.

WO200153455-A2.

26-JUL-2001.

22-DEC-2000; 2000MO-US035017.

23-DEC-1999; 99US-00471275.

21-JAN-2000; 2000US-00488725.

25-APR-2000; 2000US-00552317.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457603/49.  
DR P-PSDB; AAM25744.  
XX Isolated human polynucleotides encoding polypeptides, useful for the  
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.  
XX  
PS Claim 1; Page 578; 121pp; English.

XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
CC AAM25963. The proteins can have activities based on the tissues and cells  
CC they are expressed in, such as: antiinflammatory; antineumatic;  
CC antirheumatic; immunosuppressive; antibacterial; endocrine; cardiant;  
CC central nervous system; virucide; anti-HIV; fungicide; antitumor;  
CC cardiovascular; antianemic; antileptegant; haemostatic; vulnery;  
CC antileptegant; dermatological; antiallergic; antidiabetic;  
CC antidiabetic; cyclostatic; neuroprotective; antidepressant; nootropic;  
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
CC encoding them can be used in gene therapy, antilease therapy and vaccine  
CC production. The proteins and polynucleotides are useful for screening for  
CC agonists or antagonists of a protein and for the treatment and diagnosis  
CC of disorders associated with the activity of a protein e.g. inflammation,  
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
CC anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,  
CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
CC neurological disorders  
XX

SQ Sequence 2966 BP; 809 A; 735 C; 688 G; 733 T; 0 U; 1 Other;

Alignment Scores:  
Pred. No.: 0 Length: 2966  
Score: 3398.00 Matches: 662  
Percent Similarity: 99.70% Conservative: 1  
Best Local Similarity: 99.55% Mismatches: 2  
Query Match: 99.41% Indels: 0  
DB: 1 Gaps: 0

US-10-029-345A-109 (1-665) x AAH99685 (1-2966)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20  
DB 23 ATGGCCATGAGATGATGTAAGTGAATGTTACTAGAGGGGGGTGCTGCTGGAA 82  
QY 21 SerGlyThrGlnLysValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40  
DB 83 AGTGGAAACGAAATAAGTGGCTGCTAATGATAGCGGCGCATTTTGGAAATACATACATCC 142  
QY 41 HisIleLeuGlnAlaIleAsnIleAsnCysSerLysLeuMetLysArgLeuGln 60  
DB 143 CACATTTTGAACCCATTATATCACTGCTCCAACTTATGAAAGGAGTTGCAACAG 202  
QY 61 AspLysValLeuIleThrGlnLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80  
DB 203 GACAAAGTGTATTAACAGAGCTCATTCAGCATTCAGCGAAACATTAAGTTGACATTGAT 262  
QY 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100  
DB 263 TGCAGTCAGAGAGTTGATGTTTACGATCAAGCTCCCAAGATGTTGCTCTCTTCA 322  
QY 101 AspCysPheLeuThrValLeuLeuGlyLysGlnLysSerPheAsnSerValHisLeu 120  
DB 323 GACTGTTTCTCACTGTTACTCTGCGGTAAACGTGAGAAAGAGCTTCAACTGTTCACTG 382  
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyGluGlyLysSer 140  
DB 383 CTTCAGAGTGGGTTCGATGTTCTCTGTTGTTTCCCTGCGCTCTGTGAAGAAATCC 442  
QY 141 ThrLeuValProThrCysHisSerGlnProCysLeuProValAlaAsnIleGlyProThr 160

D	443	ACTCTAGTCCCTCACTCGATCTTCTCAAGCCTTCTCACTGTTTCCAAACATTGGGCAACC	502
Q	161	ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuLeu	180
D	503	CGAATTCTTCCCACTCTTATCTTGAGCTGCGCAGCGAGATGTCTCAACAAGAGCTGATG	562
Q	181	GlnGlnAsnGlyTILEGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe	200
D	563	CAGCGAAATGGGATGGATTGTTATGTGTTAAATGCGACCAATACCTGTGCCAAAGCTTCGACTT	622
Q	201	ILEProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysILELeu	220
D	623	ATCCCGAGTCTCACTTCTCGCTGCTGTGCTGGAATGACAGCTTTTGTGAGAAAATTTTG	682
Q	221	ProTyrLeuAspLysSerValAspPheILEguluysAlaLysAlaSerAsnGlyCysVal	240
D	683	CCGTGCTTGACCAATCAGTAGATTTCATTGGAAGAAGCAAAAGCTCCAAATGATGTGTT	742
Q	241	LeuValHisCysLysLeuAlaGlyLysSerArgSerAlaThrILEAlaILEAlaTyrILEMet	260
D	743	CTAGTGCACTGTTTATGCTGGGATCTCCCGCTCCGCGACACATCGCATGCGCTACATCATG	802
Q	261	LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProThr	280
D	803	AAGAGCATGACATCTCTTTAGATGAAGCTTACAAATTTGTGAAAGAAAAGAAAGCTTACT	862
Q	281	ILESerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLysILELysAsn	300
D	863	ATATCTCCAAACTTCAATTTTCTGGGGCAACTCTGGATGATGAAGAAGATTTAAGAAC	922
Q	301	GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGluLysProAsn	320
D	923	CAGACTGAGGACTCAGGGCGAAAGAGCAAACTCAAGCTGCTGCACTGAGAGAGCAAAAT	982
Q	321	GluProValProAlaValSerGluLysGlyGlyGlnLysSerGluThrProLeuSerProPro	340
D	983	GAACCTGTCTCTGCTGCTTCAGAGGGGTGACAGAAAAGGAGAGACCCCTCAGTCAACC	1042
Q	341	CysAlaAspSerValaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal	360
D	1043	TGTGCCGACTGTGCTACCTCAGAGGCGACAGAGCAAAAGCCGTGCATCCGCGACGCTG	1102
Q	361	ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu	380
D	1103	CCACAGCTGCCACGCGTGCAGCGCTGCTGTTAGAGGACAGCGCCGTGTACAGGCGCTC	1162
Q	381	SerGlyLeuHisLeuSerSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe	400
D	1163	AGTGGGCTGCACCTGTCCGCGACACGGCTGGAGAGCAACAATAGCTCAAGCGTTCTTTC	1222
Q	401	SerLeuAspILELysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe	420
D	1223	TCTCTGGAATTCGAATCAGTTTCATATTCAGCGACGATGGGACGATCTTACATGGCTTC	1282
Q	421	SerSerSerGluAspAlaLeuGluLysTyrTyrLysProSerThrThrLeuAspGlyThrAsn	440
D	1283	TCTCTCATCAGAAAGATGCTTTGGAAATACAAACCTTCACATCTGATGGAGCGCAAC	1342
Q	441	LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGlnThrSerPro	460
D	1343	AAGCATGCCAGTCTCTCCCTGTTCCAGAACTATGAGGACGAGACTCCGAAACCAAGTCTCT	1402
Q	461	AspLysGluGluAlaSerILEProLysLysLeuGlnThrAlaArgProSerAspSerGln	480
D	1403	GATTAAGGAGAGCCAGCATCTCCCAAGAACTGCGACGACCGCGAGGCTTTCAGACAGCCAG	1462
Q	481	SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu	500
D	1463	AGCAAGCATGTGATTCGCTCAGAACCGACGACGAGATGGCACCGCCACAAGGTCCCTTTTA	1522
Q	501	SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly	520
D	1523	TCTCCACTGCATCGAAGTGGAGCGCTGGAGACAAATTCACACACGAGCTTCTCTTTTGGCG	1582

QY	521	LeuSerThrSerGlnGlnIHisIleuThrThyLysSerAlaGlyLeuGlyLeuValGlyTyrPheHis	540		
Db	1583	CTTTCACACGACCCAGCAGACACCTTCACGAAAGCTGCTGGCTGGGCTTTAAGGGCTGGCAC	1642		
QY	541	SerAspIleuAlaPProGlnThrSerThrProSerLeuThrSerSerTyrPyrPheAla	560		
Db	1643	TCGGATATCTTGGCCCCCCCCAGACCTTACCCCTTCCCTGGACCAAGCACTGGATATTTGGCC	1702		
QY	561	ThrGlnSerSerHisIlePheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer	580		
Db	1703	ACAGAGTCTCTACACTTCTACTCTGCTCTGACCACTACAGGAGGACAGTGCAGATTACTCT	1762		
QY	581	AlaTyrSerCysSerGlnLeuProThrCysGlyLysAspGlnAlaTyrSerValArgArg	600		
Db	1763	GCTTACAGCTGACCCAGCTGCCCCCACTTGGCGAGACCAAGTCTATTTCTTGCGCAGACGG	1822		
QY	601	GlnTyrPProSerAspArgAlaAspSerArgArgSerTyrHisGlnGlnSerProPheGlu	620		
Db	1823	CAGAAAGCCAATGTACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGACCCCTTTGAA	1882		
QY	621	LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSerIleMetSerGluAsn	640		
Db	1883	AAGCAGATTTAAACCCGACAGCTGCCAATGGAATTGGAAAGAGCAATCATGTACAGAGAAC	1942		
QY	641	ArgSerArgGlnGlnIleuGlnLysValGlySerGlnSerSerPheSerGlySerMetGlu	660		
Db	1943	AGGTACAGCGGAAAGCTGGGGGAAAGTGGCAGTCAAGTCTTCTTTCGGGACAGATGGAA	2002		
QY	661	IleIleGluValSer	665		
Db	2003	ATCATTTAGTGTCTCC	2017		
RESULT 12					
ACC60521					
ID	ACC60521	standard; cDNA; 5111 BP.			
AC	ACC60521;				
XX	19-JUN-2003	(first entry)			
DE	Polynucleotide relating to the invention SEQ ID NO: 41.				
XX					
KM	Gene; ss; antiproliferative; hepatotropic; nephrotropic; antiarthritic;				
KM	antiproliferative; cardiac; cytostatic; gene therapy; liver disease;				
KM	proliferative disorder; renal failure; cardiovascular disorder;				
KM	immunological disorder; arthritis; psoriasis; congenital heart defect;				
XX	congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.				
OS	Homo sapiens.				
XX					
PN	WO200257460-A2.				
XX					
PD	25-JUN-2002.				
XX					
PF	20-DEC-2001; 2001WO-US050459.				
XX					
PR	20-DEC-2000; 2000US-0256868P.				
PR	30-MAR-2001; 2001US-0280186P.				
PR	01-MAY-2001; 2001US-0287735P.				
PR	05-JUN-2001; 2001US-0295848P.				
PR	25-JUN-2001; 2001US-0300465P.				
XX					
PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.				
PI	Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L,				
PI	Siemens N, Bol D, Schlieven G, Finger J, Todderud CG, Basolino D;				
PI	Krystek S, Mcatee P, Suchard S, Banas D,				
XX					
DR	WPI; 2002-599721/64.				
DR	P-PSDB; ABR52352.				
XX					
PT	Novel polynucleotides encoding human phosphatase polypeptides useful in				



Db	2150	ACAGAGTTCCTACACCTTCTACTCTGCGCTCCAGACCATTACGAGAGGACGACAGTTACTCT	2269
Qy	581	AlaIysSerCysSerGlnLeuProThrCysGlyIyspGlnValIlySerValIysArgArg	600
Db	2210	GCCTACAGACTCAGCCAGCTGCCCACTTGGCCGAGCCAAAGTCTATTCTGTGTCGAGGCGG	2269
Qy	601	GlnIysProSerAspArgAlaAspSerArgIysSerTTPbIsgIuGlnIysSerProPheGln	620
Db	2270	CAGAAAGCCAAAGTACAGAGCTGACTCGCGCGAGACTGGCATGAGAGAGCCCTTTGAA	2329
Qy	621	LysGlnPheIysArgArgSerCysGlnMetGlnPheGlyGlnSerIleMetSerGluasn	640
Db	2330	AAGCAGTTTAAACGACAGAAAGCTGCCCAATGTGAATTGGAGAGAGCATCATGTACAGAAC	2389
Qy	641	ArgSerArgGlnGlnLeuGlyIysValGlySerGlnSerSerPheSerGlySerMetCln	660
Db	2390	AGGTCCACGGGAAAGCTGGGGGAAAGTGGGACAGTCACTACTCTTTGCGGACGATGGAA	2449
Qy	661	IleIleGlnValSer 665	
Db	2450	ATCATTGAGGTCTCC 2464	
RESULT 13			
AA	AF30479	standard; cDNA; 2118 BP.	
XX	AA	AF30479;	
AC	AA	AF30479;	
DT	29-MAY-2001	(first entry)	
XX			
DE		Human protein phosphatase and kinase protein-4 cDNA 1234795CB1.	
XX			
KW		Protein phosphatase and kinase protein; PPHK-4; human;	
KW		gastrointestinal disorder; immune system disorder; neurological disorder;	
XX		cell proliferative disorder; cancer; diagnosis; therapy; ss.	
OS		Homo sapiens.	
XX			
FH	Key	Location/Qualifiers	
FT	CDS	25..2025	
FT		/tag= a	
FT	misc_feature	163..222	
FT		/tag= b	
FT		/note= "unique fragment"	
FT	misc_feature	1081..1140	
FT		/tag= c	
FT		/note= "unique fragment"	
XX			
PN	WO200120004-A2.		
XX			
PD	22-MAR-2001.		
XX			
PF	14-SEP-2000; 2000WO-US025515.		
XX			
PR	15-SEP-1999; 99US-0154141P.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Yue H, Tang YT, Bandman O, Hillman JL, Baughn MR, Azimzai Y,		
PI	Lu DM;		
XX			
DR	WPI: 2001-244811/25.		
DR	P-PSDB; AAB20325.		
XX			
PT	Novel human protein phosphatase and kinase proteins for diagnosis,		
PT	treatment and prevention of gastrointestinal, immune system, neurological		
PT	and cell proliferative disorders.		
XX			
BS	Claim 5, Page 97-98; 103pp; English.		
XX			
CC	The present sequence is that of cDNA encoding novel human protein		
CC	phosphatase and kinase protein PPHK-4 (see AAB20325). The cDNA was		
CC	initially identified in incyte Clone ID No. 1234795CB1, from a foetal		

	CC	Lung tissue library. Tissues that express PPHK-4 (as a fraction of total
	CC	tissues expressing PPHK-4) include gastrointestinal (0.385),
	CC	cardiovascular (0.154), nervous (0.154) and reproductive (0.154).
	CC	Diseases or conditions associated with tissues expressing PPHK-4 (as a
	CC	fraction of total tissues expressing PPHK-4) include cancer (0.692),
	CC	inflammation or trauma (0.308) and cell proliferation (0.231). The
	CC	encoded protein shows homology to mouse neuronal tyrosine threonine
	CC	phosphatase 1. The invention provides human PPHK-1 to -11 polypeptides
	CC	(see AAB20322-32) and polynucleotides (see AAF30476-86). It also provides
	CC	expression vectors, host cells, antibodies, agonists and antagonists, as
	CC	well as methods for diagnosing, treating or preventing disorders
	CC	associated with expression of PPHK, including gastrointestinal
	CC	disorders, immune system disorders, neurological disorders and cell
	CC	proliferative disorders, including cancer
	XX	
SQ	Sequence 2118 BP; 550 A; 552 C; 506 G; 510 T; 0 U; 0 Other;	
	Alignment Scores:	
Pred. No.:	0	Length: 2118
Score:	3373.00	Matches: 663
Percent Similarity:	99.40%	Conservative: 1
Best Local Similarity:	99.25%	Mismatches: 1
Query Matchn:	98.68%	Indels: 3
DB:	1	Gaps: 0
US-10-029-345A-109 (1-665) x AAF30479 (1-2118)		
OY	1	MetAlAHtsgImEtIlEGlyThrgGlnIleValThrgIArgLeuValAlaleuEnugu 20
Db	25	ATGGGCCCATGAGATATTGGAACTCAAAATTGTACTGAGAGGTTGGTGCCTTGCGGGA 84
OY	21	SergIyThrgIuLyVallleuLeuileaspSerArqProPheValGlutYrAsnThrSer 40
Db	85	AGTGAACGGAAGAAAGTCCTGCTTAATTGATAGCCGCGCATTGTGTGSAATCAATCATCC 144
OY	41	HistIleuEuGIAlilIeasnIleasnCyseSerIysIeuMerLyArgrgIeuIngIn 60
Db	145	CACATTTTGGAAAGCCATTATATCAACTGCTCCAAGCTTATAGAAGGAGTTGCACAG 204
OY	61	AsplysValleuIleThrgIuLeuIleGlnHisserAlalySHIblayValAspIIeaSp 80
Db	205	GACAAAGTGTATATTAACAAGCTCATCCAGCATTCAGCGAAACATVAGGTTCACATTGAT 264
OY	81	CysSergIuLyVallvalValalTyraSpGlnInserrGlnaspValAlaserIeusSer 100
Db	265	TGCAGTCAAGAAGGTGTGATTTACATCAAACTCCCAAGATGTGCTCTCTCTTCA 324
OY	101	AspCySPheLeuThrValleuEnugIyLysIeuGuIuLySerPheksnSerValIHisleu 120
Db	325	GACGTGTTTTCTCACACTGACTTCTGGGTAAACAGGAAAGACTTCAACTCTGTACCCTG 384
OY	121	IeuAlagIyglYPheAlagludPheSerArqCySPheProGlyIueuCysGluGlYlysSer 140
Db	385	CTTGACAGGGGGTGTGCTGAGTTCCTCGTGTGTTTCCCCTGCGCTCGTGAAGAAATCC 444
OY	141	ThrlleuValProThrCyarlleserGlnProCysIeuProValAlAsnIlegIypProTr 160
Db	445	ACTTAGTCCCTCACTGATCTTCTAGCCTTCCTTACCTGTTGCCAACATTTGGGCCAAC 504
OY	161	AfgIleLeuProAsnleuIyrIeugIyCySGlnArGaspValIleuasnlysgIuleuIle 180
Db	505	CGAATTTCTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGAGGCTGATG 564
OY	181	GlngIuaengIylEGlyTYrValIleuasnAlaserTYrThCySProLySProaspPhe 200
Db	565	CAGCAGAAATGGATGGTATGTGTAAATGACAGAAATCACTGTCCAAAGCCTGACTTT 624
OY	201	IleProGlnSerHISPhelenuArgValProValAsnAspSerPheCysGluYsIleLeu 220
Db	625	ATCCCCGAGTCTCATTTTCTGCGGTGCTGTGATGACAGCTTTGTGAGAAAATTTTG 684
OY	221	ProtPLeuAspLySerValaspHeIlegIuYsalAlasyAlaserAngIyCysVal 240

Dh 685 CCGTGGTGGACAAATCAGTAGATTTCATTGAGAAAAGCCCAATGCATGTGTT 744  
Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleMet 260  
Dh 745 CTAGTGACATGTTAGTGGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATATG 804  
Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIlysglyLysArgProThr 280  
Dh 805 AAGAGATGACATGCTTAGATGAGAGCTTACAGATTTTGAAAAGAAAAAGACTACT 864  
Qy 281 ILSerProAsnPheAsnPheLeuGlyIleLeuLeuAspTyrGlyIlyValIleValAsn 300  
Dh 865 ATATCTCCAACCTCAATTTTCTGGGCCAATCTCTGACCTATGAGAAAGATTTAAAC 924  
Qy 301 GluThrGlyAlaSerGlyProLysSerLysLeuLysLeuLysLeuGlyIlyValProAsn 320  
Dh 925 CAGATGAGACATCAGGGCCAAAGACAACTCAAGCTGCTGACCTGGAGAAAGCCAAAT 984  
Qy 321 GluProValProAlaValSerGlyIlyGlyIlyLysSerGluThrProLysSerPro 340  
Dh 985 GAACGTGCTCCCTGCTGCTCAGAGGGTGAAGAAAAGCAGAGAGCCCTCAGTCCACCC 1044  
Qy 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyIlyLysProValHisProAlaSerVal 360  
Dh 1045 TGTGCGACTCTGCTACCTCAGAGGACAGACAAAGGCCCGTGCATCCCGCAGCGTG 1104  
Qy 361 ProSerValProSerValGlnProSerLeuGluAspSerProLeuValGlnAlaLeu 380  
Dh 1105 CCAGCGTCCCGCCAGCGTGCAGCGCTCCCTTTAGAGACAGCCCGCTGGTACAGGCCCTC 1164  
Qy 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe 400  
Dh 1165 AGTGGGCTGCACCTGCTCCGACAGAGGCTGAAAGACAGCAATAGCTCAAGCGTCTTC 1224  
Qy 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420  
Dh 1225 TCTGTGATATCAAAATCAGTTTCAATATTCAGCCAGCATGTGCAGATCTTACATGCTTC 1284  
Qy 421 SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440  
Dh 1285 TCTCTCATCAGAAAGTCTTTGAACTACTCAAACTTTCCTCACTCTGGATGGGACCAAC 1344  
Qy 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSer-P 460  
Dh 1345 AAGCTATGCCAGTCTCCCTGTTCAAGAACTATCGAGAGAGACTCCCGAAACAGTTCC 1404  
Qy 460 roAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerG 480  
Dh 1405 CTGATAGAGGAGAGCCAGCATCCCAAGAAAGCTGCAGACCGCCAGCGCTTCAGACAGCC 1464  
Qy 480 InSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuL 500  
Dh 1465 AGAGCAAGCATTCATTCGGTCAAGACAGCAGCAGTGCACCGCCCAAGGTCCTTTT 1524  
Qy 500 euSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheG 520  
Dh 1525 TATCTCAGATGCAGAGAGTGGAGGTGAGGACAACTTACCAACAGCTTCTTTTTCG 1584  
Qy 520 LysLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyIleuLysGlyTyr 539  
Dh 1585 GCCTTTCCACACACCCAGCAGCAGCTTCAGAACTGCTGCGCGCCCTTAAGGGCTGG 1644  
Qy 540 HisSerAspIleLeuAlaProGlnThrSerThrProSerLeuHisSerSerTyrPhe 559  
Dh 1645 CATTGGATATCTTGGCCCCCAGACCTTCACTCCCTGACAGCAGCACTGATTTT 1704  
Qy 560 AlAThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyIlySerAlaSerTyr 579  
Dh 1705 GCCACAGAGCTTCACACTTCTACTGCTCAGGCATTCAGGAGGCAATGCAAGTTAC 1764  
Qy 580 SerAlaTyrSerCysSerGlnLeuProThrCysGlyIlyAspGlnValTyrSerValArgArg 599  
Dh 1765 TCTGCTTACAGCTGACGCGAGCTGCCCACTTGGGAGAACCAAGTCTATCTGTGGCGAGG 1824

Qy 600 ArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSerProPhe 619  
Dh 1825 CGGCAGAGCAAGCTACAGAGCTGACTCGCGCGAGCTGCGCATGAAAGAGACCCCTTT 1884  
Qy 620 GluLysGlnPheLysArgArgSerCysGlnMetGluPheGlyLysSerIleMetSerGlu 639  
Dh 1885 GAAAGCAGTTTAAAGCAGAGAGCTGCCAAATGGAATTTGAGAGAGCATCATGTCAAG 1944  
Qy 640 AsnArgSerArgGluGluLeuGlyIlyValGlySerGlnSerSerPheSerGlySerMet 659  
Dh 1945 AACAGGTCAAGGAGAAAGCTGGGAGAAAGTGGGAGTCAGTCACTGTTTGGGCGACGATG 2004  
Qy 660 GluIleIleGluValSer 665  
Dh 2005 GAATATCTGAGGTCTCC 2022  
RESULT 14  
ID ACC60560  
ACC60560 standard; cDNA; 2756 BP.  
AC ACC60560;  
XX  
XX 19-JUN-2003 (first entry)  
XX  
DE Polynucleotide relating to the invention SEQ ID NO: 113.  
XX  
XX Gene; ser; antiproliferative; hepatotropic; nephrotropic; antiarthritic;  
XX antiproliferative; cardiatic; cytostatic; gene therapy; liver disease;  
XX proliferative disorder; renal failure; cardiovascular disorder;  
XX immunological disorder; arthritis; psoriasis; congenital heart defect;  
XX congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.  
OS Mus musculus.  
XX  
XX WO200257460-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 20-DEC-2001; 2001MO-US050459.  
XX  
XX 20-DEC-2000; 2000US-0256688P.  
XX 30-MAR-2001; 2001US-0280186P.  
XX 01-MAY-2001; 2001US-0287735P.  
XX 05-JUN-2001; 2001US-0295848P.  
XX 25-JUN-2001; 2001US-0300465P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Jackson DG, Feder J, Nelson T, Muntier G, Ramanathan C, Lee L;  
XX Stiemers N, Bol D, Schieven G, Finger J, Todderud CG, Bassolino D;  
XX Krystek S, Mcatee P, Suchard S, Bannas D;  
XX  
XX MPI; 2002-599721/64.  
XX P-PSDB; ABR52385.  
XX  
PT Novel polynucleotides encoding human phosphatase polypeptides useful in  
PT the prevention or treatment of e.g. proliferative and cardiovascular  
PT disorders.  
XX  
XX Disclosure; Fig 16; 801p; English.  
XX  
XX The invention relates to a novel isolated nucleic acid comprising a  
XX polynucleotide having a nucleotide sequence selected from 40  
XX polynucleotides fully defined in the specification. The polynucleotide of  
XX the invention has antiproliferative, hepatotropic, nephrotropic,  
XX antitumor, antiproliferative, cardiatic, and cytostatic activity. The  
XX polynucleotide may have a use in gene therapy. A polynucleotide or  
XX polypeptide of the invention is useful for preventing, treating or  
XX ameliorating a medical condition, e.g. a proliferative disorder. They are  
XX also useful for treating e.g. liver disease, renal failure, immunological  
XX disorders including arthritis and psoriasis, cardiovascular disorders  
XX such as congenital heart defects and congestive heart failure, and

CC cancer. A method of the invention is useful for diagnosing a pathological  
CC condition or susceptibility to a condition in a subject. The present  
XX sequence is used in the exemplification of the invention  
SQ Sequence 2756 BP; 714 A; 675 C; 664 G; 703 T; 0 U; 0 Other;

## Alignment Scores:

Score:	0	Length:	2756
Percent Similarity:	3057.50	Matches:	594
Best Local Similarity:	93.68%	Conservative:	29
Query Match:	89.32%	Mismatches:	37
	89.45%	Indels:	5
		Gaps:	3

US-10-029-345a-109 (1-665) x ACC60560 (1-2756)

```
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db ATGCCCCATGAGTGAATGGAACTCAATGTGTACTGAGAGCTTGCTGCTCTGCGAA 428
QY 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTyrArgThrSer 40
Db AGTGAACGGAAAAAGCTGCTGCTAATGATAGCCGACCATTTGTGGAAATCAATACGCT 488
QY 41 HisIleLeuGluAlaIleAsnIleAsnCysSerIleuMetLysArgArgLeuGln 60
Db CACATTTGGAGCCATTAAATCACTGCTCCAACTGATGAAAGCCAAAGCTTCCAAACG 548
QY 489 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisIleAsp 80
Db GACAAAGTAAATTAACAGAACTAATCAACCAATCTCAAAAGCAATAGGTGACATTGAC 608
QY 61 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSer 100
Db TGCAATCAAAAGAGGAGTAAATGATGATACAGTTCAAGAAAGTGGTTCTCTGCTGCA 668
QY 609 AspCysPheLeuThrValLeuLeuGluLysLeuGluLysSerPheAsnSerValHis 120
Db GACTGCTTTCTCACTGACTTCTGGGTAAAGCTGGAGAAAGCTTCAACTGCTGCACTG 728
QY 121 LeuAlaGlyGlyPheAlaGlnPheSerArgCysPheProGlyLeuCysGluGlyLys 140
Db CTGGAGGTGGCTTGTGAGAGTTCTCTGTTGTTCCCTGGCTCTGTGAAGAAAGTCC 788
QY 729 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyPro 160
Db ACTCTAGTCCCTACTGCTGATATCTAGGCTTCTTACTGTTGGCAACATTGGGCAACT 848
QY 141 ArgIleLeuProAsnLeuTyrIleuGlyCysGlnArgAspValLeuAsnLysGluLeu 180
Db CGAATTTCTCCCAATCTCTATCTTGGCTGCCAGAGATGTCCTCAACAAGAACTGTAG 908
QY 849 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAsp 200
Db GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAsp 200
QY 909 CAAAGAAATGGAGTGGATGTGTAAATGCAACCAATACCTGTGCAAAAGCTGACTTC 968
Db CAAAGAAATGGAGTGGATGTGTAAATGCAACCAATACCTGTGCAAAAGCTGACTTC 968
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIle 220
Db ATACTGTAATCTCACTTCTGCTGAGTGCCTGGAATGACAGCTTTGTGAGAAATCTCT 1028
QY 969 ProTyrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCys 240
Db CCATGTTGGACAAAGTCTGTGATTTCAATTGAGAAAGCAAAAGCTTCCAAATGGCTGT 1088
QY 1029 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle 260
Db CTTATCCACTGCTTGTAGCTGGATCTCTGCTCGCCACACTATGCTATTTGCTTACAT 1148
QY 1089 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLeuGluLysArgPro 280
Db LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLeuGluLysArgPro 280
QY 261 AAGAGATGAGCATGTCTCTATAGTAGGCTTACAGATTTGTGAAGAAAGAAAGCACT 1208
Db AAGAGATGAGCATGTCTCTATAGTAGGCTTACAGATTTGTGAAGAAAGAAAGCACT 1208
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysIleLysAsn 300
```

```
Db ATATCCCAATTTATTTATGGCCAACTCATGAGTAAAGAGCAATTAATAAC 1268
QY 301 GlnThrGlyAlaSerGlyProLysSerLysLysLeuLeuHisIleuGlnLysProAsn 320
Db GlnThrGlyAlaSerGlyProLysSerLysLysLeuLeuHisIleuGlnLysProAsn 320
QY 1269 CAGACTGGAATGTCAGAGGCGCAAGAGCAATGAGCTCTGACTTGAACAAACCACT 1328
Db CAGACTGGAATGTCAGAGGCGCAAGAGCAATGAGCTCTGACTTGAACAAACCACT 1328
QY 321 GluProValProAlaValSerGluGlyGlnLysSerGluThrProLeuSerProPro 340
Db GluProValProAlaValSerGluGlyGlnLysSerGluThrProLeuSerProPro 340
QY 1329 GAGCCGCTGCTGACACCTCAGAGGCGGATGGAAAGTGAAGTCTGCTCAGTCCACCC 1388
Db GAGCCGCTGCTGACACCTCAGAGGCGGATGGAAAGTGAAGTCTGCTCAGTCCACCC 1388
QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSer 360
Db CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSer 360
QY 1389 TGTGCCAACTCG--ACTCGGAGGATCATGAGGCAAAAGCTTGTGATCTTGA----- 1439
Db TGTGCCAACTCG--ACTCGGAGGATCATGAGGCAAAAGCTTGTGATCTTGA----- 1439
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
Db ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
QY 1440 --AGTGTCCCGCTTACAGCCGTCACTTGAAGACAGTCCGTGGTACAGGGCTC 1496
Db --AGTGTCCCGCTTACAGCCGTCACTTGAAGACAGTCCGTGGTACAGGGCTC 1496
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe 400
Db SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe 400
QY 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
Db SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
QY 1557 TCTCTGATATCAAACTGTTTCATATTCAGCCAGATAGGCGCGCTTCTTACACGGCTTC 1616
Db TCTCTGATATCAAACTGTTTCATATTCAGCCAGATAGGCGCGCTTCTTACACGGCTTC 1616
QY 421 SerSerSerGlnAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
Db SerSerSerGlnAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
QY 1617 --TCGTACAGAGAGGCTTTAGACTGCAAACTTCTGCCACACTGATGGAGCAAC 1673
Db --TCGTACAGAGAGGCTTTAGACTGCAAACTTCTGCCACACTGATGGAGCAAC 1673
QY 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
Db LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
QY 1674 AAGCTGTGCAGATTCTCCCGCTTACAGAGTATCAGAAAGAGTCCAGAGCAAGCCG 1733
Db AAGCTGTGCAGATTCTCCCGCTTACAGAGTATCAGAAAGAGTCCAGAGCAAGCCG 1733
QY 461 AspLysGluGluLysIleLeuProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db AspLysGluGluLysIleLeuProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
QY 1734 GATAGAGAGAGGCGCCACATCCCAAGAGCCCAACCTTCCAGGCTTGTGAGAGCCAG 1793
Db GATAGAGAGAGGCGCCACATCCCAAGAGCCCAACCTTCCAGGCTTGTGAGAGCCAG 1793
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
Db SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
QY 1794 GTCAACAGCTTGCACTAGTGAAGAACCGGAGTAGTGAGCCACCCAGAGGCTTCTTC 1853
Db GTCAACAGCTTGCACTAGTGAAGAACCGGAGTAGTGAGCCACCCAGAGGCTTCTTC 1853
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisPheLeuPheGly 520
Db SerProLeuHisArgSerGlySerValGluAspAsnTyrHisPheLeuPheGly 520
QY 1854 TCGGCATGTCATGCGAGCGGAGGTGTAAGAGAACATTAACCAATCACTCTTTTGGC 1913
Db TCGGCATGTCATGCGAGCGGAGGTGTAAGAGAACATTAACCAATCACTCTTTTGGC 1913
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540
Db LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540
QY 1914 CTTTCCACAGCCAGCAACCTTCAACAGTCTGAGGCTTGGCTTCMAAGGCTGGCAC 1973
Db CTTTCCACAGCCAGCAACCTTCAACAGTCTGAGGCTTGGCTTCMAAGGCTGGCAC 1973
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
Db SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
QY 1974 TCAGATATTTGGTCTCCCAAGTCTTGCCTTGCCTTGCACAGCAATGTGTATTTGCT 2033
Db TCAGATATTTGGTCTCCCAAGTCTTGCCTTGCCTTGCACAGCAATGTGTATTTGCT 2033
QY 561 ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerAlaSerTyrSer 580
Db ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerAlaSerTyrSer 580
QY 2034 ACGGAGCCTTCACTGTTGACTGCTTCAAGCCATCTATGAGGCAACAGAGATTACTCT 2093
Db ACGGAGCCTTCACTGTTGACTGCTTCAAGCCATCTATGAGGCAACAGAGATTACTCT 2093
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
Db AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
QY 2094 GCTTACAGCTGTGGCCAGCTGCGCCACTTGGACAGTACCAAAATCTTGTGTTGTAAGCGG 2153
Db GCTTACAGCTGTGGCCAGCTGCGCCACTTGGACAGTACCAAAATCTTGTGTTGTAAGCGG 2153
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGluGluLysProPheGlu 620
Db GlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGluGluLysProPheGlu 620
QY 2254 CAGAAAGCTTACTGACAGAGCTGACTCGAGGCGGAGCTGCGATGAAAGAGAGCCCTTTGAA 2213
Db CAGAAAGCTTACTGACAGAGCTGACTCGAGGCGGAGCTGCGATGAAAGAGAGCCCTTTGAA 2213
QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAsn 640
Db LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAsn 640
QY 2214 AAGCAATTTAAACCAAGAGCTGCCAATGGAATTTGAGAGCAATTAATGTCCGAGAAC 2273
Db AAGCAATTTAAACCAAGAGCTGCCAATGGAATTTGAGAGCAATTAATGTCCGAGAAC 2273
QY 641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
```

DB 2274 AGGTCCAGGAGGAGCTGGGCAAGTGCGACGACGATCTTCCGCGACGATGAG 2333  
QY 661 |||||leuValSer 665  
DB 2334 ATCATCGAGGCTCT 2348  
RESULT 15  
ABK48378  
ID ABK48378 standard; cDNA; 3332 BP.  
XX  
AC ABK48378;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE cDNA encoding human DSP-16 alternative form protein.  
XX  
KW Human; dual-specificity phosphatase-3; DSP-16; autoimmune disease;  
KW mitogen-activated protein kinase; MAP; Duchenne muscular dystrophy;  
KW cancer; graft-versus-host disease; allergy; metabolic disease;  
KW abnormal cell growth; abnormal cell proliferation; contact inhibition;  
KW cell cycle abnormality; anchorage independent cell growth; apoptosis;  
KW intercellular adhesion; DSP-16 modulator; chromosome 12p; gene; se.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS /tag= a /product= "Human dual-specificity phosphatase-3 (DSP-16)  
FT alternative form protein"  
XX  
PN MO200226997-A2.  
PD 04-APR-2002.  
XX  
PF 25-SEP-2001; 2001WO-US030124.  
XX  
PR 26-SEP-2000; 2000US-0235487P.  
XX  
PA (CEPT-) CEPTYR INC.  
XX  
PI Luche RM, Wei B;  
XX  
DR WPI; 2002-315802/35.  
XX  
DR P-PSDB; AAU79159.  
XX  
PT New DSP-16 polypeptide, useful for identifying modulators of its  
PT activity, which can be used in the treatment of disorders such as  
PT Duchenne muscular dystrophy, or cancer.  
XX  
PS Claim 56; Fig 3; 87pp; English.  
XX  
CC The present invention relates to a new polypeptide, DSP-16, having a 665  
CC amino acid sequence, given in the specification, or a variant having at  
CC least 50 % identical residues, which retains the ability to  
CC dephosphorylate an activated mitogen-activated protein (MAP) kinase. The  
CC invention can be used for identifying agents which modulate DSP-16  
CC activity, for modulation of a proliferative response in a cell, survival  
CC of a cell, or differentiation of a cell. The cell displays contact  
CC inhibition of cell growth or anchorage independent growth and may display  
CC altered intercellular adhesion. The agent may modulate apoptosis, or the  
CC cell cycle. The identified modulators can be used to treat Duchenne  
CC muscular dystrophy, cancer, graft-versus-host disease, autoimmune  
CC diseases, allergies, metabolic diseases, abnormal cell growth, abnormal  
CC cell proliferation, and cell cycle abnormalities. The present nucleic  
CC acid sequence is that of the human dual-specificity phosphatase-3 (DSP-  
CC 16) gene located on chromosome 12p. This sequence encodes the human DSP-  
CC 16 alternative form protein of the invention  
XX  
SQ Sequence 3332 BP; 909 A; 805 C; 823 G; 795 T; 0 U; 0 Other;  
Alignment Scores: 0 Length: 3332  
Pred. No.:

Score: 3048.50 Matches: 607  
Percent Similarity: 91.44% Conserved: 2  
Best Local Similarity: 91.14% Mismatches: 1  
Query Match: 89.19% Indels: 56  
DB: 1 Gaps: 1  
US-10-029-345A-109 (1-665) x ABK48378 (1-3332)  
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20  
DB 562 ATGGCCCATGAGATGATGGAACTCAATTTGTTACTGAGAGGTTGGGCTCTGGGAA 621  
QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40  
DB 622 AGTGAACGGAAAGAAAGTCTGCTTATTTGATAGCCGGCACTTTGTGGAATACATACCTC 681  
QY 41 HisIleLeuGluAlaIleLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 60  
DB 682 CACATTTTGGAAAGCCCTTATATCACTGCTCCAAAGCTTATGAAAGCGAGTTGCAACAG 741  
QY 61 AspLysValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80  
DB 742 GACAAAGTGTAAATACAGAGCTCATTCCAGCAATTCAGCGAAACATTAAGTTGACATTGAT 801  
QY 81 CysSerGlnLysValValValValValValValValValValValValValValValValVal 100  
DB 802 TGCAGTCAGAAAGTGTGATTTGATTCGATCAAGCTCCCAAGATGTGCTCTCTCTCA 861  
QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheLeuValHisLeu 120  
DB 862 GACTGTTTCTCACTGATCTTGGGTAACCTGGAGAGAGCTTCAACTGTTCACTG 921  
QY 121 -IleAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGluGlyLys 140  
DB 922 CTG----- 925  
QY 140 rThrLeuValProThrCysIleSerGlnProCysLeuProValAlaIleValIleGlyProth 160  
DB 925 ----- 925  
QY 160 rArgIleLeuProAsnLeuThrLeuGlyCysGlnArgPheValLeuAsnLysGluLeu 180  
DB 926 -----CAGAGCTGAT 936  
QY 180 eGlnGlnAsnGlyrIleGlyThrValLeuAsnAlaSerThrThrCysProLysProAspPhe 200  
DB 937 GCAGCAGAAATGGATGTTATGTATGTTAAATGCGAGCAATATCTGTCCAAGCCTGACTT 996  
QY 200 eileProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLe 220  
DB 997 TATCCCGAGTCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056  
QY 220 uProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240  
DB 1057 GCGGTGTTGCAAAATCACTGATATTTCACTTGAAAGCAAAAGCCTCCAAATGATGTGT 1116  
QY 240 IleValHisCysLeuAlaIleLysSerArgSerAlaThrIleAlaIleAlaThrIleMe 260  
DB 1117 TCTAGTGCATGTTTGTAGCTGGGATCTCCCGCTCCGACCATGCTATTCCTTACATCAT 1176  
QY 260 tLysArgMetAspMetSerLeuAspGluAlaThrArgPheValLysGluLysArgProth 280  
DB 1177 GAAGAGATGAGATGCTCTTTAGTATGAGCTTACAGATTTGTGAAGAAAGAAAGAAAGCTTAC 1236  
QY 280 rIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspThrGluLysIleLysAs 300  
DB 1237 TATATCTCCAAACTCAATTTCTGGGCAACTCTGCACTATGAGAAAGAAAGTTAAAGAA 1296  
QY 300 ngInThrGlyAlaSerGlyProLysSerLysLeuLysLeuLysLeuLysLeuLysProAs 320  
DB 1297 CCAGACTGAGAGCATCGAGGCGCAAGAGCAAACTCAAGCTGCTCACCCTGAGAGAGCCAAA 1356  
QY 320 ngIuProValProAlaValSerGluGlyGlnLysSerGluThrProLeuSerProPr 340

Db 1357 TGAACCTGTCCTGCTGCTCAGAGGCTGAGACGAAAAACGAGACGCCCTCAGTCCACC 1416  
QY 340 oCYsAlaAspSerAlaThrSerGluAlaIaIaGlyGlnArgProValHisProAlaSerVa 360  
Db 1417 CTGTGCCGACTCTGCTACTCTCAAGGACGACGACGACGACGACGACGACGACGACGACG 1476  
QY 360 lProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAla 380  
Db 1477 GCCCAGCTGCTGCCAGGCTGACGCGTCTGTTAGAGGACAGCCGCTGTACAGCGCT 1536  
QY 380 uSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerLeuGlyLeuValArgSerPh 400  
Db 1537 CAGTGGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1596  
QY 400 eSerLeuAspIleuValSerValSerValSerValSerValSerValSerValSerVal 420  
Db 1597 CTCTCGATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1656  
QY 420 eSerSerSerGluAspAlaLeuGluTyrTyrTyrProSerThrThrLeuAspGlyThrAs 440  
Db 1657 CTCTCATCAGAAAGTCTTGTGAATACTACAAACCTTCACTACTGATGGGACCAA 1716  
QY 440 nLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPr 460  
Db 1717 CAAAGCTATGCCAGTTCTCCCTGTTCAAGAACTATCGAGACGACTCCGAAACCAAGTCC 1776  
QY 460 oAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerG 480  
Db 1777 TGATTAAGGAGGAAAGCAGCATCCCAAGAGCTGCAGACCGGCTTACAGACAGCCA 1836  
QY 480 nSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500  
Db 1837 GAGCAGGAGATTGCAATTGCTCAGAACCAAGCAGGCTGCGACCGCCAGAGTCCCTTTT 1896  
QY 500 uSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheG 520  
Db 1897 ATCTCAGCTGCATCGAAGTGGAGGCTGAGGACAAATTACACACAGCTTCTTTTCGG 1956  
QY 520 yLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrPh 540  
Db 1957 CCTTCCACGAGCCGACGACCTCAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2016  
QY 540 sSerAspIleLeuAlaProGluThrSerThrProSerLeuThrSerSerTyrTyrPheAl 560  
Db 2017 CTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACGAGCTGGTATTTTGC 2076  
QY 560 aThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSe 580  
Db 2077 CACAGAGCTCTCACACTTCTGCTCTGCTCAGCCATCTACGAGGACGTGCCAGTTACTC 2136  
QY 580 rAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgAr 600  
Db 2137 TGCCACAGCTGCGAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2196  
QY 600 gGlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGluGluSerProPheG 620  
Db 2197 GCAGAAAGCAAGTACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2256  
QY 620 uLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAs 640  
Db 2257 AAGACAGTTTAAAGCAGAAAGCTGCCAAATGGAATTGAGAGAGCATCATGTCAGAGAA 2316  
QY 640 nArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetG 660  
Db 2317 CAGGTCAAGGAGAGCTGGGAGAAAGTGGCAGTCAAGTCTTTCGGGCGACATGGA 2376  
QY 660 uIleIleGluValSer 665  
Db 2377 AATCATTGAAGTCTCC 2392

Job time : 77 secs